

## FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA  
CCACGCGTCCGGGCGGAGCAGCACGCGCCGAGGACCTGGAGTCCGGCTGCGTCTTCCCG  
CAGCGCTACCCGCCATGCGCGCTGCCGCGCCGGGCGCGCTGGGGCTCCTGCCGCTTCTGCTG  
CTGTGCCGCCCGCGCCGAGGGCCGCCAAGAAGCCGACGCCCTGCCACCCGGTGCCGGGGGCT  
GGTGGACAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACA  
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGTGAGAGATC  
CTGGAGGGGCTGTGCAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA  
GCACCTGGAGGCGCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTTT  
GTGTGAAGACACTGAAAGTGTGTCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGC  
CAGGGCGGATCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGAGATGGGAGCAGACA  
GGCGCAGCGGTCTCTCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGTCACTGACTGCATGG  
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC  
TGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCT  
GGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCTCCCTGCAGCGCTG  
CGCAGTTCTGTAAAGACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTG  
GGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA  
CGGACAGTGTGCAGATGTGGACGAGTGTCTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACG  
AAAAGTGTACAATACTCCAGGGAGCTACGTCTGTGTGTGTCTGACGGCTTCGAAGAAACG  
GAAGATGCTGTGTGCCGCCGCGAGAGGCTGAAGCCACAGAAGGAGAAAGCCCACACAGCT  
GCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTACCCTTTAAATTATTTCAGAAGGATGTCC  
CGTGAAAAATGTGGCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGCGGGGAGAGGCTGC  
CTGTCTCTAACGGTTGATTCTCATTGTCTCCTTAAACAGCTGCATTTCTTGTTGTCTTTA  
AACAGACTTGTATATTTTGATACAGTTCTTTGTAATAAAAATTGACCATTGTAGGTAAATCAGG  
AGGAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGC  
TTGGCCGCCATGGCCCACTTGTATTATTCAGCTTATAATGGTTACAATAAAGCAATAGCA  
TCACAAATTTCACAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTGTGCCAACTC  
ATCAATGTATCTTATCATGTCTGGATCGGGAATTAATTCCGCGCAGCACCATGGCCTGAAAT  
AACCTCTGAAAGAGGAACCTTGGTTAGGTACCTTCTGAGGCGGAAGAACCAGCTGTGGAATG  
TGTGTCAAGTTAGGGTGTGGAAGTCCCCAGGCTCCCAGCAGGCAGAAGTATGCAAGCATGC  
ATCTCAATTAGTCAGCAACCCAGTTTT

## **FIGURE 2**

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDATAKNFGGGNTAWEEKTL SKYESS EIRL  
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCSPGTYGPDCLACQGGSGRQPCSG  
NGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNETHS ICTACDESKTCSGLTNRDCGECEVGWVLDE  
GACVDVDECAAEPPPCSAQAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKE C I S G Y A R E H G Q C A D V D E C S L A E K T  
CVRKNENCYNTPGSYVVCVCPDGFEEETEDACVPPAEAEATEGESPTQLPSREDL

### **Signal peptide:**

amino acids 1-24

### **N-glycosylation sites.**

amino acids 190-194 and 251-255

### **Glycosaminoglycan attachment sites.**

amino acids 149-153 and 155-159

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 26-30

### **Casein kinase II phosphorylation sites.**

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343  
and 349-353

### **Tyrosine kinase phosphorylation site.**

amino acids 303-310

### **N-myristoylation sites.**

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and  
313-319

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 308-320

### **EGF-like domain cysteine pattern signature.**

amino acids 166-178

### **Leucine zipper pattern.**

amino acids 94-116

## FIGURE 3

CAGGTCCAAC TGCACCTCGGTTCTATCGATTGAATTC CCGGGGATCCTCTAGAGATCCCTC  
GACCTCGACCCACGCGTCCGCCAGGCCGGGAGGCGACGCGCCAGCGCTCTAAACGGGAACA  
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCCAGGTTTCGCTAGGTGCG  
GCACGAGGAGTTTTCCCGGCAGCGAGGAGGTCTGAGCAGCATGGCCCGGAGGAGCGCCTTC  
CCTGCCGCCGCGCTCTGGCTCTGGAGCATCTCTGTGCTGCTGGCACTGCGGGCGGAGGC  
CGGGCCGCCGAGGAGGAGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCA  
TAGGATTGGAAGAAGATATCTCTGATTGTTTCAGAGGGGAAAATGGCACCCTTTACATCATGAT  
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCATGAATTTTAC  
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCCTGTCTTGCCTCCCTGGATA  
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAAGGCA  
TCAGTTTGTTCAGATTGGTTTCCCATGTCTTGAAAAACAGGATGGGGTGGCAGCATTTGAAGT  
GGATGTGATTGTTATGAATTCCTGAAGGCAACACCATTCTCAAACACCTCAAATGCTATCT  
TCTTTAAACATGTCAACAAAGCTGAGTGCCAGGCGGGTGCCGAAATGGAGGCTTTTGTAAAT  
GAAAGACGCATCTGCGAGTGTCTGTATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTTG  
TACCCACGATGTATGAATGGTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCACCTG  
GATTTCTATGGAGTGAATGTGACAAAGCAAACCTGCTCAACCCTGCTTTAATGGAGGGACC  
TGTTTCTACCTTGGAAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG  
CAATATGCCCAACAACCTGTGCAAAATGGAGGTAAATGCATTGGTAAAAAGCAATGTAAAGTGT  
CCAAAGGTTACCAAGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGACAT  
GGAACCTGCCATGAACCCAAACAATGCCAATGTCAAGAAAGTTGGCATGGAAGACACTGCAA  
TAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGCGCGCCAGCTCAGGCAGC  
ACACGCCTTCACTTTAAAAAGGCCGAGGAGCGCGGGATCCACCTGAATCCAATTACATCTGG  
TGAACTCCGACATCTGAAACGTTTAAAGTTACACCAAGTTTCATAGCCTTTGTTAACTTTCA  
TGTTTGAATGTTCAAATAATGTTTACATTACACTTAAGAATAC TGGCCTGAATTTTATTAGCT  
TCATTATAAATCACTGAGCTGATTTACTCTTCTTTTAAAGTTTCTAAGTACGCTGTGTAG  
CATGATGGTATAGATTTTCTGTGTTCACTGCTTTGGGACAGATTTTATATTATGTCAATTGA  
TCAGGTTAAAAATTTTCAGTGTGTAGTTGGCAGATATTTCAAATTACAATGCATTTATGGT  
GTCTGGGGGCAGGGGAACATCAGAAAGGTTAAATTTGGGCAAAAATGCGTAAGTCACAAGAAT  
TTGGATGGTGAGTTAATGTTGAAGTTACAGCATTTTCAGATTTTATTGTTCAGATATTTAGAT  
GTTTGTGTACATTTTAAAAAATTGCTCTTAATTTTAAACTCTCAATACAATATATTTTGACC  
TTACCATATTTCCAGAGATTCAATATAAAAAAATAAATTACACTGTGTGTAGTGGCATTT  
AAACAATATAATATATTTCAAACCAATGAAATAGGGAATATAATGTATGAATTTTGTGAT  
TGGCTTGAAGCAATATAATATATTTGTAACAAAAACACAGCTCTTACCTAATAAACATTTTAT  
ACTGTTTGTATGTATAAAATAAAGGTGCTGCTTTAGTTTGTGGAAAAAATAAATAAATAA  
AAAAAATAAATAAATAAATAAAGGGCGCGCAGCTCTAGAGTCGACCTGCAGAAGCTTGGC  
CGCCATGGCCCAACTGTTTATTGCAGCTTATAATG

## **FIGURE 4**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFFAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSE GK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNITLQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCSKPVC
EPGCGAAGTCHPEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERDRP
PESNYIW
```

### **Signal peptide:**

amino acids 1-28

### **N-glycosylation site.**

amino acids 88-92, 245-249

### **Casein kinase II phosphorylation site.**

amino acids 319-323

### **Tyrosine kinase phosphorylation site.**

amino acids 370-378

### **N-myristoylation sites.**

amino acids 184-190, 185-191, 189-195, 315-321

### **ATP/GTP-binding site motif A (P-loop).**

amino acids 285-293

### **EGF-like domain cysteine pattern signature.**

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

## FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTGCGCAGAGCCAGGAGGCGGAGGCGCGCGGGGCCAGCCTGGG  
CCCCAGCCCCACACCTTACCAGGGGCCAGGAGGCCACCAATGTGGGCGATGTCCACTGGGGCTAC  
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCAGCAGGGTCGTGGGCGCCGG  
GAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGACCGGGAGGCCCGGTACTGCCAGGA  
GCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTACCTGGGCGCCATCT  
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCGCTGACTTCTGGGACTTC  
TGCTCGGCTGGCCACCCCCCTTTTCCCCCGATCCAAGGATGTATGCATGGAGGTCTGTATCTA  
TCCAGTCTTGGGAACGTACTGGGACAACGTGAACCGTTGCACCTGCCAGGAGAACAGGCACT  
GGCATGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCCTGG  
GAACCACAGCGCCTTCTGGGGCATGACCTGGATGAAGGGCATTTCGTACCGCCTGGGCACCA  
TCCGCCCATCTTCCCTCGGTATGAACATGCATGAAATTTATACAGTGTCTGAACCCAGGGGAG  
GTGCTTCCACAGCCCTTCGAGGCCCTCTGAGAAGTGGCCCAACCTGATTCATGAGCCTCTTGA  
CCAAGGCAACTGTGCAGGCTCTGGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT  
CAATCCATTCTCTGGGACACATGACGCCTGTCTGTGCGCCCCAGAACCCTGCTGTCTTGTGAC  
ACCCACAGCAGCAGGGGCTGCCGCGGTGGGCGTCTCGATGGTGCCTGGTGGTTCTGCGCTCG  
CCGAGGGGTGGTGTCTGACCACCTGTACTCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCC  
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCACTGCC  
CACTGCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCT  
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA  
TGGAGGTGCATGAGGACTTCTTCTATACAAGGAGGGCATCTACAGCCACAGCCAGTGAGC  
CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTCAAGATCAAGGATGGGG  
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTCGCGCCAACTCCTGGGGCC  
CAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGC CGGCGTCAATGAGTGCACATCGAG  
AGCTTCGTGCTGGGCGTCTGGGGCGCGTGGGCATGGAGGACATGGGTCACTCACTGAGGCTG  
CGGGCACACGCGGGGTCCGGCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCAATG  
GGGCGGTGACCCAGCCTCGCCCGACAGAGCCCGGGGCGCAGGGCGGGCGCCAGGGCGCTAAT  
CCCGGCGCGGGTCCGCTGACGACGCGCCCCGCTGGGAGCCGCGGGCAGGCGAGACTGGCG  
GAGCCCCAGACCTCCAGTGGGGACGGGGCAGGGCTTGGCTGGGAAGAGCACAGCTGCAG  
ATCCAGGCCTCTGGCGCCCCACTCAAGACTACCAAAGCCAGGACCTCAAGTCTCCAGC  
CCCAATACCCCAACCCCAATCCCGTATTCTTTTTTTTTTTTTTTTAGACAGGGTCTTGTCCG  
TTGCCAGGTTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTCA  
AGTGACCTCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACCACCACACCTGGC  
TAATTTTTGTATTTTTGTAAAGAGGGGGGTCTCACTGTGTTGCCAGGCTGGTTTCGAAC  
CTTGGGCTCAAGCGGTCCACCTGCCTCCGCTCCCAAGTGCTGGGATTGCAGGCATGAGCC  
ACTGCACCCAGCCCTGTATTCTTATTCTCAGATATTTATTTTTCTTTTCACTGTTTAAAA  
TAAACCAAAGTATGTATAAAAAAAA

## **FIGURE 6**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPGLGLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDCC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPFPIQGCMMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDGP
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### **N-glycosylation site.**

amino acids 78-82, 161-165

### **Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

### **N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

### **Amidation site.**

amino acids 26-30, 318-322

### **Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

## **FIGURE 7**

AGGCTCCTTGGCCCTTTTTCACAGCAAGCTTNTGCNATCCCGATTGCTTGTCTCAAATCCA  
ATTCTCTTGGGACACATNACGCCTGTCCTTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC  
CAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCCTGGTGGTTCCCTGCCGTCGCCGAGG  
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC  
CCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCACTGCCCACTGC  
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC  
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG  
TGCATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG  
AGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAG

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## FIGURE 8

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT  
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG  
GAGCAGTGCTGGACCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG  
CAGCTTGAAGTGCCTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT  
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTT  
GCCGTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG  
CCCCGCTGCAGCCCACTCGGGTGTGGTGCCCCAGGCCCTCTGTGCCACTCCTCACAGACCTG  
GCCCAGTGGGAGCCTGTCTGGTTCCCTGAGGCACATCCTAAACGCAAGTCTGACCATGTATGT  
CTGACCCCTGTCCCCACCCCTGACCCCTCCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA  
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCCCTCCAACCCCTCTGCTGCTGTTTC  
CATGGCCCAGCATTCTCCACCCCTTAACCCCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT  
CCCTGCCCCACCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGACCCAGCA  
GGGGAAGGCACTCAGGAGGGCCCATAAAGGCTGAGATGAAGTGACTGAGTAGAACTGGA  
GGACAAGAGTCGACGTGAGTTCTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA  
GGGGCCAGGCCTCACATTCTGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT  
AATAAACACCTGTTGGATAAGCCAAAAAAA

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## **FIGURE 9**

MTHRTTTWARRTSRAVTPTCATPAGPMPGCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT  
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHPDPPMALSRTPTRQISSSDT  
DPPADGPSNPLCCCFHGFAPSTLNFVLRHLFPQEAFPAHPIYDLSQVWSVVSFAPSRGQALRRAQ

**Signal peptide:**

amino acids 1-47

**N-glycosylation site.**

amino acids 31-35, 74-78, 84-88

**Casein kinase II phosphorylation site.**

amino acids 22-26, 76-80

**N-myristoylation site.**

amino acids 56-60

**Amidation site.**

amino acids 70-74

[illegible]

CCACGCGTCCGAACCTCTCCAGCGATGGGAGCGCGCCGCTGCTGCCAACCTCACTCTGT  
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTAGTACGTGAGGGACCCAGGGCGCCATGACC  
GACCAGCTGAGCAGGCGCGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAAGTGGCAAGCA  
CGTGCAAGTACACGGGCGTTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGC  
TCATAGTGGAGACGGACACGTTTGCGAGCCGGTTTCGCATCAAAGGGGCTGAGAGTGAGAAG  
TACATCTGTATGAACAAGAGGGGGCAAGCTCATCGGGAAGCCAGCGGGAAGAGCAAAGACTG  
CGTGTTTCACGAGACTCGTCTGGAGAACAACTATACGGCCTTCCAGAACGCCCGCGCAGGAG  
CTGTGTTCACTGAGCCTTACGCGAGGGGCGGCCCCGCGAGCTTCCCGCAGCCGCCAGAAC  
CAGCGCGAGGGCCCACTTCATCAAGCGCCTCTACCAAGGCAGCTGCTGCCCTTCCCCAACACGC  
CGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCACCGCCGGACCAAGCGCACAC  
GGCGGCCCCAGCCCCCTCACGTAGTCTGGGAGGCAGGGGGCAGCAGCCCCGCGGCGCCTCCC  
CACCCCCTTCCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCC  
GAGGGAGGACCTTGAGGGCCGCGAAGCATCCGAGCCCCAGCTGGGAAGGGGAGGCCGGTG  
CCCCAGGGGCGGTGCGCAGTCCCCCTTCCGGACGGGTGGCAGGCCCTTGAGAGGAACT  
GAGTGTCAACCCTGATCTCAGGCCACAGCCTCTGCCGGCTCCAGCCGGGCTCTGAAGCC  
CGCTGAAAGGTACGCGACTGAAGGCCTTGAGACAACCGTCTGGAGGTGGCTGTCTCAAAA  
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCAGCCCCCAAACCTCCTCTGGCTAGACTGTA  
GGAAGGTGACTTTGTTTGTTTGTGTTTTCAGGAAAAAGAAAGGGAGAGAGAGGAAATAG  
AGGGTTTGCCACTCTCACTTCCACAGCCAGGCCCTGCACCCCAACCCCACTCCAGGCC  
CGGATAAAACCACTTTTCTCTGC

## **FIGURE 11**

MGAARLLPNLTLCQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRISATAEDGNKFVKLIVETDTFGSRVRIKGAESEKYICMNRGKLGKPSGKSKDCVFTEIVLENNYTAFQNRHGEWFMATFRQGRPRQASRSRQNRBAHFVKRLYQGQLPFPNHAEEKQKQFEFVGSAPTRRTKRTRRPQPLT

### **Signal peptide:**

amino acids 1-22

### **N-glycosylation site.**

amino acids 9-13, 126-130

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

### **Casein kinase II phosphorylation site.**

amino acids 65-69

### **Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

### **N-myristoylation site.**

amino acids 69-75, 188-194

### **Amidation site.**

amino acids 58-62

### **HBGF/FGF family signature.**

amino acids 103-128

[illegible]

ACTTGCCATCACCTGTGTGCCAGTGTGGAAAAATTTCTCCCTGTTGAATTTTTCGCACATGGAG  
GACAGCAGCAAAAGAGGGCAACACAGGCTGTATAAGACAGGACAGCAGGGAGATATTATTAC  
CATACGCCCTCCAGGAGCTTCCCTCTAGCTGGAGTTCTGGAGCTTCAACAGAAACCCATCCAGT  
CATTTTGATTTTGTCTGTTTATTTTTTTTTTCTTTCTTTTCTTTCCACCAATGTATTTTAT  
TTCCTGATCTCAGAAATGGGGCTACAGACCAAAAGTGGCCAGCATGGGGCTTTTTTCTCT  
GAAGTCTTGTCCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCC  
CTAGTGTGTGCGCCCTGCAGCAGGAACCTTGCTCTACTGTAAATGAGCGAAGCTTGACCCTAGTG  
CCTCTTGGGATCCCGGAGGGGCTAACCGGTACTCTACCTCCACAAACCAAAATTAATAATGCG  
TGGATTTCTGCAGAACTGCACAATGTACAGTCCGGTGCACCGGCTTACCTGTATGGCAACC  
AACTGGAGCGAATTTCCCATGAACCTTCCCAAGAAATGTAGAGTCTCCATTTCAGGAAAAAC  
AATATTGCAGACCAATTTCCAGGGCTGCTCTTGGCCAGCTCTGAAGCTTGAAGAGCTGCACCT  
GGATGACAACTCATATTCCACAGTGGGGGTGGGAAGCGGGGCTTCCGGGAGGCTATTAGCC  
TCAAATTTGTGTTTTGTCTAGAAGTCACTGAGCAGTGTGCTCTTGGGGCTCTGTGTGGAC  
TTGCAAGAGTGTAGAGTGGATGAAAAATCGAATTGCTGTATATCCGACATGGCCTTCCAGAA  
TGGCAGAGCTTGGAGCGTCTTATTGTGGAGCGGAACCTCTGCACCAACAGGGGTATTGCCG  
ACTCCACCTTCCAGCTCTCACCAGCTCACAAGAACTTCAAATGTACGTATTTCTGCTGTCC  
CACCCTCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTTTCAGGACCAACAGAT  
AAACCAACATTTCCCTTGACAGCCTTCAAATCTTCGTAAGCTGGAACGGCTTGGATATATCCA  
ACAACCAACTCGGTGTGCTAGCTCAAGGGTTTGTGAATCTCTCCAACCTGAAGCATGCT  
ACTGCTCGGAATAACCTTGTGTTTTGTGATCGAGTATAAATGGGTGCAGAAATGGTCTCAA  
ATATATCCCTTCTCATCTCAACGTGCGGGTTTATGTGCCAAGTCTCGAAGTGTGCGG  
GGATGGCCGCTGAGGGAATTAATATGAATCTTTTGTCTGTCCCAACACGACCCCGGCCGTG  
CTCTCTTCCACCCAGCCCAAGTACAGCTTCTCCGACCACTCAGCGCTCCCAACCTCTCTAT  
TCCAAACCTTAGCAGAACTACAGCCTCCAACTCCGACCACTCGAAATTTCCACAGATT  
CTGATCGGATGTCAGAGAAAGATGACCCCACTTATTCTGAACGGATCAGCTCTCTATC  
CATTTTGTGAATGATACTTCCATTCAAGTCAGTGGCTCTCTCTCTTCCCGGTATGGCATA  
CAAACTCATAGTGGTGAATAATGGGCCAGGTTTAGTAGGGGCGATCGTTGACGAGCGCATAG  
TGCTGAGGTGGAAGCAACACTGACGCTGGTTAACTTAGAGCCCGGATCCACCTCATCGGAT  
TGTTTGTGTCACCTGGATGCTTTTTAACTACGCGCGGTAGAAGACCACTTTGTTACAGGGC  
CACCACCCATGCCTCTTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA  
CGTCCCAACGATGGCTGCCCTTCTCTGCTGCGGGCTTGATCGGGGGCGCGGTGTATATT  
GTGCTGGTGGTCTTGCTCAGCGCTTTTGTGTGGCATATGCAAAAAAGGGGCGGTACATCTT  
CGAGAAGTGAATAATCAACCGGGGCGCGCGAAAGATGTTATTGCGAGGACGACCAACAGAA  
ACGCAACTCTCATCTGGAGATGACAGAACCAAGTTTTCAGATCGTCTCTTAAATAACGAT  
CAACTCTTTAAAGGAGATTTCAGATGCAAGCCCAATTACACCCCAATAGGGGGCATTAATTA  
CACAGATGCCATATCCCCAAGCAACATGCATATGCAACGAGCGCTGCAGACACTGGAGC  
ACTGCCATACCTGACCGCAGGAGCCAGCGGTTATCAAGGCGGACCAATAGACTCTTGAGAA  
CACACTCTGTGTGTGCACATAAAGACACGCGAGATTACATTTGATAAATGTTACACAGATGCAT  
TTGTGCAATTTGAATATCTGTGAATTTATAACGGTGTACTATAATGGGATTTAAAAAGTG  
CTATCTTTTCTATTTCAGTTTAAATTAACACAGTTTGTGAATCTTTGCTTTTAAATCTT

## **FIGURE 13**

MGLQTTKWPSHGAFFLKSWLIISGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP  
EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFFPMNLPKNVRVLHLQENNIQTI  
SRAALAQLLKLEELHLDNISITVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR  
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD  
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN  
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMVRELNMMNLLSCPTTTPGLPLFTP  
APSTASPTTQPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGRERVTPPI SERIQLSIHFVND  
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL  
DAFNRYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL  
LSVFCWHMHKKGRYTSQKWYKYNRRKKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG  
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVDPLEHCHT

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 542-561

**N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

**Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

**Tyrosine kinase phosphorylation site.**

amino acids 319-328

**N-myristoylation site.**

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639

**Amidation site.**

amino acids 581-585

**Leucine zipper pattern.**

amino acids 164-186

**Phospholipase A2 aspartic acid active site.**

amino acids 39-50

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ACTTCGACGACGCGCGCGCGGCGGAGACAGAGCGAGACAGCGAGCTGGGGCTCGCTCTCTCTCCACGAGCG  
 ATCCGACGAGGAGACGCGCGCGCTCGGCGGAGCGAAGAGGCCAGCAGAGAAACCGGGTGGCTCGCGCCCTGCC  
 TCGCTTCACGAGCGACGCGCGCTCGAGCCTTGCCCTCTTGCTCGCTTGAAAATGGAAAAGATGCTCGCAGGCT  
 GCTTTCTGCTGATCTCTCGACAGATGCTCTCTCTCTCGCGGAGCGCAGGAGCGGTCAGTGGGAGTCCATCT  
 CTGGGGGACGACGCTCGGACCCACCCGACGAGCGCTTTGGAGATGTCCTGGAGAACCGGGGACGACCC  
 TGGTTTCTCATTCATTGACAGCTCTCGAGTGTCAACAACCCATGACATAGCAAAGTCAAGGAGTTCATGTCGGACA  
 CTTTGCAATTCTTGGACATTGTGCTGTAGTGCACCGAGTGGGCTGCTCCAAATGGCGAGCATCTCGAAGTAT  
 AGTTTCTCCCTCAAGACCTTCAAGAGGAATCGAGGTGGAGCGTGTCTTCAAGAGGATCGGGCATCTGTCCAC  
 GCACCAATGATGGTGGCTGGCCATCAGTAGTGCCTGAACAATCGCATCTCAAGAACGAGGGGGCCCGCCCTGGA  
 GGGAGATTTGGCCACGGGTCAATATGATGCTGACAGATGGAGACCTCAGGATCTCCGTGGCAGGAGTGGCTGCTA  
 AGCAACGGGACACGGGCATCTTAATCTTTGGCAATGGTGGGGCAGGTAGACATTCAACACTTGAAGTCATTGG  
 GGAATGAGCCCATGAGGACCATGTCTTCTGTGGCCAAATTACAGCAGATAGAGACGCTGACCTCGTGTCTTGA  
 AAGAGAAGTTGTACGCGGCCCAATGTGTGAGCAGCACTGGAGCATAGCTTGCCCACTCTGCACTCAAACTCCG  
 GCTCATAGCTCTCGAGTGCAGAACAGGCTCATTTCTCAACTGGATAGAGGACGACTCTGCAAGATCCAGGATCTGT  
 GTGCCATGGAGGACCAACACTGTAGACAGCTGTGTGGAATGTGGCGGCTCTCGTCTGCGCATGTACAGTGT  
 GCTACGCCCTGGCTTGAGATGGGAAGAGGTGTGTGGCTGTGGACATGCTGCTCTCAAAAACCAAGATGTGAAAC  
 ATGAGTGTGTAATGTGTATGGCTCTTAACTTTTGCCAGCTCATGAAGATTTGCTCTTAACCCAGATGAAAAAC  
 CGTGCACAGGATCAACTACTGTGCATGAAACAACCGGCTGTGAGCATGTAGCTGCTCAATCTGAGGAGAGCT  
 ACTTACGCGCTGCCACCTGGTCACTGTGCACCACTGAATGGCAAACTCGACGCGATGGACCATCTGTGCAC  
 AGGAGACCACTGGCTGTGAGCAGCTGTGTGTGAACCGGAGATTCCTTCGCTGCCAGTGTCTGAGAGGTTCC  
 TCATCAACAGGAGCACTAAGACTGCTCCGGGTGGATATGCTCTGTGAGTAGCAATGTTGTGAATATCTCT  
 GTGTCAACATGGACAGCTCTTGCGGTGACGTGCTCTGAGGAGCACTGCTCGCCAGGATGGGAACGCTGTGT  
 CAAATTGGACATCTTGATCTTGCCGACCAACCGTTTGAACATTCTGTCTTAAGCATGAAGATTCGTTTGTGT  
 CCGAGTCTTGAAGGTATATATCTGACGTGAAGTGGAAAACCTGCAGAAAGAAATCTCTGCCAAGCTTAG  
 AACTGTGCTTGAAGTTAATTGTGTGAACAGTAGCACTATACAGTGTGCGAGTCTTGAGGGATTCGCGCTG  
 CTGAGGATGGGAAGCTCTGCCAAGGAAGATGTCTGCAATACACCCCAATGTGTCGAACCAATTTGTGTTA  
 ATAAATGGAAGCCCAATTGACCTGGCTGTGTTGTGATGTAGTGTCAAGTCTTGGAGAGAGATTTGAAGTCTG  
 TGAGCAGCAATTGTGACATGGAATATAGATTCTTGAAATTTCCCCAACCGCGCTCGATGTGGGCTGTCCGAT  
 GCTATGGAAGCCCAATTGACCTGGCTGTGTTGTGATGTAGTGTCAAGTCTTGGAGAGAGATTTTGAAGTCTG  
 TGAGCAGCAATTGTGACATGGAATATAGATTCTTGAAATTTCCCCAACCGCGCTCGATGTGGGCTGTCCGAT  
 GCTATGGAAGCCCAATTGACCTGGCTGTGTTGTGATGTAGTGTCAAGTCTTGGAGAGAGATTTTGAAGTCTG  
 ACATGAATAATCATGGGAAGAGGCTCTATGACTGGGCTGGCCCTGAAACCATGTGTGAGAGAGGTTTACCAAG  
 GAGAGGGGCGGACGCCCTTTCCAAAGAGTGGCCAGAGCGCACTTGTGTACCGACGAGCGGCTCAGGAT  
 ACGTCTTCGAGTGGGCGCATGAAGCGCAAGGCGCAATGGATACATATGTACTGTCTGGGTAGGAAAGGCCAT  
 GAGGAGGACATCAAGAGATTTGCTCTGAGCCCAATGAACCAAGCATCTTCTATGTCGGAAGCTTCAGACAAATG  
 ATGAGATGAAGTGAATAACTGCAAGAAAGGCATCTGTGAAGCTTAGAGAGTCCGATGGAGACAGGATCTCCAG  
 CAGGGAGCACTGCCAAAACCGTTCACAGGCCAACAGATCTGAGCGAGTCACTCAATAATATCAAGACCTACTC  
 CTGTTTCTAATTTTGCACTGGAACACAGATATCTGTTTGAAGAGACCAATCTTTCAGGCTTACACAAAGCTT  
 CCCATTCAACAAATCTCAGAAGCCCTTTGGAAGAAAAACAGTCAATGCAATGTGAAACCTTATAATGT  
 TCCAGAACTCTGCAACAGGAGATGAGAAAAATTAACACACGCGCTAGAGAAATGACACAGAGATGGAGGCC  
 TGGAAAATCGCTTGAGATACAGATGAAGATAGAATTCGCGACCAATTTGATGACTATGTATCAGGATATCAAT  
 GAACCGCATCGAGAGCGCCAAAGCTCAGGCTATGTGTAATCAAGATGTGTGAATGTAACCAATCAGTACATGA  
 GAACCTGGTTTGGCACAACCAAGACAGAGACAGAGTATACAACTGTGATATACTTAGGAAAACCAATCTCT  
 TCAAGATCTCAAGATGAATTTACAGGTTGAGATGAATTAAGTACTCAAGGTATTGTTATATATCTGTGGAAC  
 AACTGCTCTGCTCTCACTCGCTCTTAGTGTGTAAGTGAATCTTAGCATATAGTAAGTATGACAGTCTATTCT  
 CTATGAACACTGGCCATAGGAATGCTGTTTTTTGAAGTGTGATCTTATGATATGATATGATGATGATCTAG  
 CATAAAATCATGAGACATATGACTTTGGGAACAGTGTGAACTTTTATACATTAATAAATCACCACTTAG

## **FIGURE 15**

MEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGRHARTHPTQTALLESSCENKRADLVFII  
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTPKRKSEVERAV  
KRMRLHSTGTMGTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD  
TGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTLSVVFQKKLCTAHMCSSTLEHN  
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCQEQLCVNVPGSFVCQCYSGYA  
LAEDGKRCVADVYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCRINYCALKNKPCC  
EHECVNMEESSYYCRCHRGYTLDPNGKTCRSVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLLI  
NEDLKTCSRVDYCLLSDHGCEYSVCVNMDRSFACQCPGHHVLRSDGKTCAKLDSICALGDHGCE  
HSCVSSSEDSFVCQCFEGYILREDGKTCRRKDVCAIDHGCEHICVNSDDSYTCBCELEGFRLA  
EDGKRCRRKDVCKSTHHGCEHICVNNGNSYICKCEGFVLAEDGRRCKKCTEGPIDLVFVID  
GSKSLGEENFEVVKQFVTGIIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA  
HMKYMGKGSMTGLALKHMFERSFTQEGGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN  
GITMYAVGVGKAIEEELQEIASEPTNKHFLFYAEDFSTMDEISEKLKKGICEALESDGRQDS  
PAGELPKTVQQPTSESEPTINIQDLLSCSNFAVQHRYLFEBDNLRLRSTQKLSHSTKPSGSP  
EEKHDQCCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 115-119, 606-610, 892-896

**Casein kinase II phosphorylation site.**

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,  
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,  
781-785, 819-823, 866-870

**N-myristoylation site.**

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,  
639-645, 690-696, 752-758, 792-798

**Amidation site.**

amino acids 314-318, 560-564, 601-605

**Aspartic acid and asparagine hydroxylation site.**

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,  
540-546, 581-587

## FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCTCG  
GCACCTGCAGGTCGGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGC  
CATGATTTCCCTCCCGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA  
GTGCCCTCGGCCCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCCGCAACCGGTTGCAG  
GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGGAGGTGTCTTC  
ATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAGAGGATC  
AGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC  
ATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAGACTCTGCCCCCTA  
CAGTGCTCCGTGAATGTGAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT  
TAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT  
GTGGGGGCAACGTGACCTTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA  
GTGGGATCGGCAGCTTCATCCTTCCAGACTTCTTTGCACCAGCATTAGATGTCTATCCGTG  
GGTCTTTAAGCCTCACCAACCTTTCTGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC  
AATGAGGTGGGCATGCCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCTGGAGCTGC  
AGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC  
TCTTGTAACACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC  
ATTGCTCCCGACCTGCCCTGGCCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCT  
TTCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCAGGCCCTGGTGCAT  
TGACCCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTACCAAGACTGCCACGACAGAT  
GGGCCCCACCCTCAACCAATATCCCCCATCCCTGGTGGGTTTCTTCTCTGGCTTGAGCCG  
CATGGGTGCTGTGCTGTGATGTGTGCTGCCAGAGTCAAGCTGGCTCTCTGGTATTGATGAC  
CCCACCACTCATTTGGCTAAAGGATTTGGGGTCTCTCCTTCTTATAAGGGTCACCTCTAGCAC  
AGAGGCTGAGTCATGGGAAAGAGTCACACTCTGACCCTTAGTACTCTGCCCCACCTCTC  
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCAGGAGACAGAAGGAGAAGAGGA  
AGTGGATCTGGAATTGGGAGGAGCTCCACCCACCCTGACTCCTCCTTATGAAGCCAGCTG  
CTGAAATTAGCTACTACCAAGAGTGAGGGGCAGAGACTTCAGTCACTGAGTCTCCAGGC  
CCCTTGATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGT  
ATTGATATAACCTGTGAGCTGGCTTGGTTAGGTTTTACTGGGCAGAGGATAGGGAATCTC  
TTATTAAACATAACATGAATAATGTGTGTTTTCATTGCAAATTTAAATAAAGATACATAA  
TGTTTGATGAAAAA



## **FIGURE 17**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS  
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSTKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY  
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCSPRSKPAVQYQ  
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNTLEVSTGPGAA  
VVAGAVVGTILVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLFPWPKSSDTISKNGTL  
SSVTSARALRPPHGPFRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSR  
MGAVPVMVPAQSQAGSLV

### **Signal peptide:**

amino acids 1-29

### **Transmembrane domain:**

amino acids 245-267

### **N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

### **N-myristoylation site.**

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99

[illegible]

## **FIGURE 19**

MKRLPLLVVFSTLLNCSYQNC'KTPTCLPNAKCEIRNGIEACYCNMGFSNGVITICEDDNEC  
GNLTQSCGENANCTNTEGSIYCMCVPGFRSSSNQDRFITNDGTVC IENVNANCHLNDVNCIAA  
NINKTTLTKIRSIKEPVALLQEVYRNSVTDLSPTDIIITYIEILAESSLLGYKNNTISAKDTL  
SNSSTLTBFVKTVNNFVQRDTFVVWDKLSVNHRRTHLTKLMHTVEQATLRISQSFQKTTEFDT  
NSTDIALKVFFFDSYNMKHIHPHMNDGDYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS  
SSDNFLLKPQNYDNSEEEERVISSVISVSMSSNPPTLYELEKITFTTSLHRKVTDYRSLCAF  
WNYSPDTMNGSWSSGCELTYSNETHTSCRCNHLTHFAILMSSGPSIGIKDYNILTRITQLG  
IIISLCLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSEIIAGL  
LHYFFLAFAWMCIEGIIHLYLIVVGVIYKNGFLHKNFYIFGYLSPAVVVGFSAALGYRYYGT  
TKVCWLSTENNFIWFSFIGPACLIILVNLLAFGVIIYKVFRTAGLKPEVSCFENIRSCARGA  
LALLFLLGTTWIFGVLHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEYYRLFKNV  
PCCFGCLR

### **Signal peptide:**

amino acids 1-19

### **Transmembrane domain:**

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,  
648-664

### **N-glycosylation site.**

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,  
188-192, 249-253, 381-385, 395-399

### **Glycosaminoglycan attachment site.**

amino acids 49-53

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 360-364

### **Casein kinase II phosphorylation site.**

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,  
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,  
346-350, 608-612

### **Tyrosine kinase phosphorylation site.**

amino acids 36-44, 669-677, 670-678

### **N-myristoylation site.**

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,  
434-440, 480-486, 521-527

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 75-87

## **FIGURE 20**

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGNG  
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTTATATTATAAGAGTAT  
TGGTCCCTTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAAATTTATGATAATTCT  
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTAGTCTCAATGAGCTCAAACCCACCCAC  
ATTATATGAACTTGAAAAAATAACATTTACATTAAAGTCATCGAAAGGTCACAGATAGGTATA  
GGAGTCTATGTGGCATTTTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG  
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA  
TTTTGCAATTTTGATGTCCTCTGGTCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA  
GGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTTACCTTC  
TGTTCTTCAGTGAAATTCAAAGCACCAGGA

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[illegible]

GCTCCACGACCAAGAACTCTCGGGGGCGCTGCGCGGTGGGGAGGAGTTCCTCCGAAACCCGCGCC  
 CTAAGCGAGGCCCTCTCTCTCCCGCAGATCCGAACGGCTCTGGGCGGGTCACCCCGGCTGGGA  
 CAAGAAGCCGCCCGCTGCTGCTCCGGGCCCCGGGAGGGGCTGGGCTGGGGCGGAGGCGG  
 GGTGTGAGTGGGTGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGTCTCGGG  
 TGTCTTGGGCACTACCCGTGGGGCCGCTAAGGCGCTACTATAAAGCTGCGCGGCCGAG  
 CCGCGCGCCGCTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCG  
 GGCACTCAGACGCCCGCAGCGCATCCCGCTCGCCGCCAGCTCTCCGCAACCCCATTCGCCGG  
 AGCTGCGCCGAGAGCCCGGAGGAGTGCCATGGCGGAGCGGTGTGTGGTGTCCAGTATAGG  
 ATCTCTGGCCGCGCTCTGGCTGGCCGCTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGC  
 CCACGTGCACTACGGCTGGGGCGACCCCATCCGCTCGGGCACTGTGTACACTCCGCGCCCC  
 ACGGGCTCTCCAGCTGCTTCTGCGCATCGTGCCGACGGCGTCTGTGGACTGCGCGGGGG  
 CAGAGCGCGCAGATGTTGCTGGAGATCAAGGCAGTCGCTCTCGGACCGTGCCCATCAAGGG  
 CTGTCACAGCGCTGCGGTACTCTCTGCATGGGGCCGACGGCAAGATGCAGGGGCTGCTTCAGT  
 ACTCGGAGGAAGACTGTGCTTTCGAGGAGAGATCCGCCAGATGGTACAATGTGTACGGA  
 TCGAGAAGACCGCCCTCCGGTCTCCCTGAGCAGTGCCAAACCGGCGAGCTGTACAAGAA  
 CAGAGGCTTTCTTCTCACTCTCTCAITTTCTGCCCATGTGCCCATGTGTCTGAGAGGCTGT  
 AGGACCTCAGGGGCCACTTGAATCTGACATGTTCTCTTGCGCCCTGGAGACCGACAGCATG  
 GACCCATTGGGGCTTGTCACGGCATGGAGGCGGTGAGGAGTCCACCTCTTGGAGAAGTAACT  
 GAGCAACTGCGCGGGCTCTTCTCACTGCGCCAGGGGCTGTGTGATCTCGACGCTGGGGGACG  
 TGCTTCTACAAGAACAGTCTTGAGTCCACGTTCTGTTTGTAGCTTTAGGAAGAAACATCTAGAA  
 GTTGTTACATATTCAGAGTTTTCATTGCGAGTGGCGATTCTTAGCCAAATAGACTTGTGTGAT  
 CATAACATGTGAAGCTGTGATGCTGCCAGCGTGTGCTGGGGCCCAATTCTGTCTCTCGA  
 GTTTGTCTGGAAGAAGCTGTGCACTGTCTCAGTTCTGCTTGAATACCTTCATCTGATGGGGAAC  
 TCACTTCTTTGGAAAAATCTTATGTCAAGCTGAAATTTCTAAATTTTCTCATCACTT  
 CCCAGGACCGCCGAGAAGACAGGCAGTAGTTTAAATTTACGGAACAGGTGATCCACTCTGTA  
 AAAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCACTTCTCAGGG  
 ACCATTTGCCCTTCCCAAATCCCTCAGGCCAGAACTGACGTGAGCAGGAGTGGCCACAGC  
 GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAGTGTGAAATTTCCC  
 CTGAGGCCAGCTCTGTCTATGATGCTGTCTCTGAGAATAACTGCTGTCCCGGTGTCACTGCT  
 TTCACTCTCCGAGCCACCAGCCCTTGCCCACTCACTAGCTCCCCATGGATTTGGGGCTCT  
 CCGAGGCCCCCCACTTTATGTCAACTGCACTTCTTTGTCAAAAATCAGGAAAGAAAGAAAT  
 TTGAAGACCCCAAGTCTGTGCAATATCTGCTGTGTGGAAGACGGGGGAAGACTAGAAAC  
 CCTTTCCCAGCAGCTTGGTTTTCCAACATGATATTTATGAGTAATTTATTTTGTATGTACA  
 TCTCTATTTTCTTACATATTTATGCCCCAAATTAATTTATGTATGTAACTGAGGTTTG  
 TTTTGTATATTTAAATGGAGTTTGGTTTG

## **FIGURE 22**

MRSGCVVHVHVLWLAGLWLA VAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI  
RADGVVDCARGQSAHSLLEIKAVLRRTVAIKGVHVSRYLCMGADGKMQGLLQYSEEDCAFEE  
EIRPDGYNVYRSEKHLPLVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD  
MFSSPLETDSMDPFGLVTGLEAVRSPSF EK

### **Signal peptide:**

amino acids 1-22

### **Casein kinase II phosphorylation site.**

amino acids 78-82, 116-120, 190-194, 204-208

### **N-myristoylation site.**

amino acids 15-21, 54-60, 66-72, 201-207

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 48-59

## FIGURE 23

CCCAGAAGTTCAAGGGCCCCCGCCTCCTGCGCTCCTGCCGCCGGGACCCCTCGACCTCCTCA  
GAGCAGCCGGCTGCCGCCCCGGGAAGATGCGCAGGAGGAGCCGCCACCGCCTCCTCCTGCTG  
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCCAAA  
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCAA  
AGAAGACTGTTTTCTCCAGATTAGAGTGGAAGAACTGGGTCGGAGTGTCTCCTTTGTCTAC  
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCATATCCG  
GATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG  
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT  
CCATCATGTGAAGTACCCCTCTTCTGCTCTGAGTGGAACGTGGGTAGAGCTACGATGTCAAGA  
CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAGGATGGCATCCGTTTGCTAGAAA  
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACACAATGAATACAAAACCTGGAAC  
CTGCAATTTAATACTGTTTTCCAACTGGACACTGGAGAATATTCCTGTGAAGCCCGCAATTC  
TGTTGGATATCGCAGGTGTCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA  
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCGGTTTGTGGCCTTGGTGTATGCTAT  
GCTCAGAGGAAAGGCTACTTTTCAAAGAAACCTCCTTCCAGAAGAGTAATTCTTCATCTAA  
AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGAAGG  
CCGCGCGGGCGGATCACGAGGTCAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAACCC  
CATCTCTACTAAAATACAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCAGCTGC  
TTGGGAGACAGGAGAATCACTTGAAACCCGGGAGCGGAGGTTGCAGTGAGCTGAGATCACGC  
CACTGCAGTCCAGCCTGGGTAAACAGAGCAAGATTCCATCTCAAAAATAAAATAAATAAATA  
AATAAATACTGGTTTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTC

## **FIGURE 24**

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRL  
WKKLGRSVSFVYYQQTQLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQNLEED  
TVTLEVLVAPAVPSCBVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQST  
NSSYTMNTKTGTTLQFNTVSKLDTGEYSCEARNVSGYRRCPGKRMQVDDLNISGIIAAVVVVA  
LVISVCGLGVCYAQRKGYFSKETSFKSNSSSKATTMSENVQLTPVIPALWKAAGGSRGQEF

### **Signal peptide:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 130-144, 238-258

### **N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

### **Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

### **N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

### **Amidation site.**

amino acids 226-230



## FIGURE 25

GACATCGGAGGTTGGGCTAGCACTGAAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAG  
AAAGAAGAGGAAGATGTTGGGCAACATTTATTAAACATGCTCCACAGCCCGACCCTGGCCAT  
CATGCTGCTATTPCCTGCAAACTACTGAAGAAGCATGGGATTAAATATTTTACTTCTTAAATAA  
ATGAATTACTCAATCTCCTATGACCATCTATACATACTCCACCTCAAAAAGTACATCAATA  
TTATATCATTAAAGGAAATAGTAACCTTCTCTTCTCCAATATGCTATGCATTTTGGACAATG  
CAATTGTGGCACTGGCACTTTATTTCAGTGAAGAAAAAAGCTTTGTGGTCTATGGCATTTCATCA  
TTTGACAAATGCAAGCATCTTCTTATCAATCAGCTCCTATTGAACTTACTAGCATCTGACTG  
TGGAACTCTTAAGGGCCATTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT  
CCGAATTCATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG  
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGTTTACACCCAGATCCATTTAT  
ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGCTTTTAACTTTCCAGCCAGATTGCC  
AGCTAACACACAGATTCTTCTCCTACAGACTAACAAATATTGCAAAAATTGAATACTCCACAG  
ACTTTCAGTAAACCTTACTGGCCTGGATTATCTCAAAACAATTTATCTTCAGTCACCAAT  
ATTAATGTAAAAAAGATGCCCTCAGCTCCTTTCTGTGTACCTAGAGGAAAAACAAACTTACTGA  
ACTGCCTGAAAAATGTCTGCTCCGAACTGAGCAACTTACAAGAACTCTATATTAATCACAACT  
TGCTTTCTCAAAATTTCACTGGAGCCCTTATTGGCCTACATACTTCTTCCGACTTCTCACTC  
AATTCAAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGTATGCTCTTCCAATCTAGAGAT  
TCTGATTGATGGGAAAAATCCAATTTATCAGAATCAAAGACATGAACCTTTAAGCCTCTTATCA  
ATCTTCGAGCCCTGGTTATAGCTGGTATAAACTCACAGAAATACCAGATAACGCCCTGGTT  
GGACTGGAAAACTTAGAAAGCATCTCTTTTACGATAACAGGCCTTATTAAAGTACCCCATGT  
TGCTCTTCAAAAAGTTGTAATCTCAAAATTTTGGATCTAAATAAAAACTCTATTAATAGAA  
TACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAAGATTGGGGATAAATAATGCCCT  
GAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAGC  
TACTAACCAACCTAGATTGCTTTACATTACCCCAATGCATTTTTCAGACTCCCCAAGCTGG  
AATCACTATGCTGAAACAGCAATGCTCTCAGTGCCCTGTACCATTGGTACCATTGAGTCTCTG  
CCAAACCTCAAGGAAATCAGCATAACAGTAACCCCATCAGGTGTGACTGTGTTCATCCGTG  
GATGAACATGAACAAAACCAACATTCGATTTCAGGAGCCAGATTCACTGTTTTCGCTGGACC  
CACCTGAATTCGAAGGTGAGAATGTTTCGGCAAGTGCAATTCAGGGACATGATGGAATTTGT  
CTCCCTCTTATAGCTCCTGAGAGCTTTCCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGT  
TTCCTTTCACTGTAGAGCTACTGCAGAACCAAGCCTGAAATCTACTGGATAACACCTCTG  
GTCAAAAACCTTGGCTAATACCTTGACAGACAAGTTCTATGTCATTCTGAGGGAACACTA  
GATATAAATGGCGTAACCTCCCAAAGAAGGGGTTTATATACTTGTATAGCAACTAACCTAGT  
TGGCGCTGACTTGAAGTCTGTTATGATCAAAAGTGGATGGATCTTTTCCACAAGATAACAATG  
GCTCTTTGAATATTAATAAGAGATATTCAGGCCAATTCAGTTTGTGGTGTCTGGAAGCA  
AGTTCTAAAATCTCAAAATCTAGTGTTAAATGGACAGCCCTTGTCAAGACTGAAAAATCTCA  
TGCTGCGCAAGGTGCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC  
CATCAACTGAGTATAAAATTTGATTGATATCCCACCATCTATCAGAAAAACAGAAAAAA  
TGTGTAATGTCAACCAAAAGGTTTGACCCCTGATCAAAAAGAGTATGAAAGAATAATAC  
CACAACTATGAGCCTGTCTTGAGGCCCTTCTGGGGATTATGGTGTGATATGTCTTATCA  
GCTGCTCTCTCCGAAATGAACTGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG  
AAACCAACCTTTGCATTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAAGCAGGAAA  
AGAAAAAGTACATCACTGAAAGTAAAAGCAACTGTTATAGGTTTACCAAACAAATATGTCCT  
AAAAACCAACAGGAACCTACTCCAAAATGAAC

## **FIGURE 26**

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT  
FPARLPANTQILLQLQTNNAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKMPQLLSVYLE  
ENKLTTELPEKCLSELNLQELYINHNLSTISPGAFIGLHNLRLHLNSNRLQMINSKWFDA  
LPNLIELMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRL  
IKVPHVALQKVYNLKFPLDLNKNPINRIRRGDFSNNMLHLKELGINNMPELISIDSLAVDNLPD  
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNLSNALSALYHGHTIESLPNLKEISIHSPNIRC  
DCVIRWMNMNKTNIRFMPEPDSLFCVDPPEFQGGQNVQRVHFRDMMEICLPLIAPESFPSNLNV  
EAGSYVSFHCRAABQPEIYWITPSGQKLLPNTLTDKFVHSEGTLDINGVTPKEGGLYTC  
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSSVKWTAFFV  
KTENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE  
YEKNNTTTLMACLGGLLGIIGVICLISCLSPENMCDGGHSYVRNYLQKPTFALGELYPLIN  
LWEAGKEKSTSLKVKATVIGLPTNMS

### **Signal sequence:**

amino acids 1-22

### **Transmembrane domain:**

amino acids 633-650

### **N-glycosylation site.**

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629

### **Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

### **Tyrosine kinase phosphorylation site.**

amino acids 570-579

### **N-myristoylation site.**

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708

### **Cell attachment sequence.**

amino acids 277-280

## FIGURE 27

GCCCCGGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG  
CTGCAGCCTTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAAACCTTTAC  
CACGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCAGCATGAATCT  
GGTAGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCTACAAAGTTTTGTTCTTA  
TGATACTGTGCTTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCTCTGGG  
GGTTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCTCTCTGA  
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTAAAG  
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCAT  
GCCTTCAAAGGAGTAGCTGAAACCTTGCGAGACTCTGGACTTGTCCGACAATCGGATTCAAAG  
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACACCCCTGGC  
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC  
AACGTGATCTGTAAAAAGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCTCAATGCTGC  
CAACGACGCTGACCTTTGTAACTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCA  
TGTTTGGCTGGTTCACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG  
GATGCCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA  
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAACTGACTGTCTATTGAGAAAGAAAGAAA  
GTAGTTTGCGATTGCAGTAGAAATAAGTGGTTACTTCTCCCATCCATTGTAAACATTTGAA  
ACTTTGTATTTTCAGTTTTTTTTGAATTATGCCACTGCTGAACTTTTAAACAACTACAACA  
TAAATAATTTGAGTTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGT  
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTT  
AATTTAAAGCAAATAAAAGCTTAACTTTGAAACCATGGGAAAAAAAAAAAAAAAAAAAAACA

## **FIGURE 28**

MNLVDLWLTRSLSMCILLQSFVLMILCFHSASMCPKGCLCSSSGGLNVTCSNANLKEIPRDL  
PPETVLLYLDNSQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVATLQTLDDLSDNR  
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPF  
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVYVYVRQNQEDARRHLEYLKSLSRQKK  
ADEPDDISTVV

### **Signal sequence:**

amino acids 1-33

### **Transmembrane domain:**

amino acids 205-220

### **N-glycosylation site.**

amino acids 47-51, 94-98

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 199-203

### **Casein kinase II phosphorylation site.**

amino acids 162-166, 175-179

### **N-myristoylation site.**

amino acids 37-43, 45-51, 110-116

[illegible]

ACCGAGCCGAGCGGAGCGAAGGGCGCGCCGAGATGCAAGTGTAGCAAGAGGATGCTGGCGGGG  
GGCGTGGAGGAGCATGCGCCAGGCCCTCTGGGCTGTGGCAGGCCCATCTCTGTGTGTGT  
GGGCTCATGTGTGTGTCAGGCTCGGCCACGGGTGCGCCCGGCTGCGAGTGTCTCCGCAAG  
ACCGCGCTGTGTGTGCCACCGCAAGTGTCTTTGGGCAAGTCCCGAGGGGCTCCCCACGAG  
ACGCGCCCTGTGGACCTTAGGCAAGAACCGCATCAAAACGCTCAACAGGACGAGTTTCGCCAG  
CTTCCCGCACTTGGAGGAGTGTGGAGCTCAACGAGAACTCGTGAGCGCCGTGGAGCCCGGG  
CCTTCAACAACTCTTCAACCTTCGCGAGCTGTGGGTCTTCGCGACCAACCGCTGAAGTCAT  
CCGCTAGGCGTCTTCACTGGCTCAGGAACTGACCAAGAGGACATCAGCGAGAACAGAT  
CGTTATCCTACTGGACTACATGTTTCAGGACCTGTACAACTCAAGTCACTGGAGTGGCG  
ACAATGACCTGTCTACATCTCTCAACCGCGCTTCAGCGCGCTCAACAGGCTGGAGCAGCTG  
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCAGAGGCGCTGTCCCACTGCACGGCTG  
CATGTCTCTGAGGCTCGGGCACTCAACATCAATGCCATCGGGATACTCTTCAAGAGGC  
TGTACCGACTCAAGGCTTGGAGATCTCCCACTGGCGCTACTTGGACACCATGACCAACCA  
TGCCTCTACGGCTCAACCTGAGCTCCCTGTCCATCACACATGCAATCTGACCGCTGTGCC  
CTACTCGCGCTCGGCCACTGATGTATCTCCGCTTCTCAACTCTCTTCAACACCCATCA  
GCACATTGAGGGCTCATGTTGCTAGTGTCTCGGCTCAGGAGATCAGCTTGGTGGCG  
GGGCACTGGCCGTGTGGAGCCCTATGCTCTTCGCGCGCTCAACATCTGCGGCTGTCTCAA  
TGTCCTTGGCAACCAAGCTGACCACTCGGAGGAATCAGTCTTCACTCGTGGGCAACCTGG  
AGCACTACTCTTGGACTTCAACCCGCTGGCTGCGACTGTGGCTCTGTGGGTGTCTCCGG  
CGCGCTGTGGCGCTCAACTCAACCGGCAAGCAGCCAGTGGCGCGCCAGCCGAGTTTGTCCA  
GGCCAGGAAGTTCAAGAGCTTCCCTGATGTGCTACTGCCCAACTACTTCACTGCGCGCG  
CCGCACTCGGGAACCGAAGGCCCAAGAGTGTTTGTGGCAGAGGGCCACACGGTGCAGTTT  
GTGTGCGGGGCGATGGCAGCCCGCGCGCQATCTCTGGCTCTCACTCCCGCAAGACCT  
GGTCTGACGCAAGAGCAATGGCGGCTCAGAGTCTTCCCTGATGGCAGCTGGAGTGTGCGT  
ACGCGCAGGTACAGGACAGGCAAGTCACTGTGATCGCGGCCAAGCGGGCGGCAACGAC  
TCCATCGCGCGCACTGCATGCGCAGCTACTCGCCGAGCTGGCCCCATCAGCGCCCAAC  
GACCTTCGCTTTCATCTCAACAGCGCGGCGAGGAGAGGCCAACAGCAACCGCGCACTG  
TGCCTTTCCCTCTGCATACCAAGACCTCATCATCGCCACCACCTGGGCTTCATCTCTTTC  
CTGGGCGTGCCTCTTCTTCTGCTGTGTGTCTGTTTCTCTGAGCGGGGCAAGGCAACAC  
AAAGCACAACATCGAGATCGAGTATGTGCCCGAAGTTCGAGCGCAGGCATCAGTCTCCGCG  
ACGCGCCCTCGAAGTTCAACATGAGATGATATGAGGCGCGGGGGGGGCGGAGCCCGCG  
GGCGCGGGGCGAGGGAAGGGGCTGTGTGCCACTGTCTACTCTCAGTCTCTTCCACTCT  
CTCCCTACCTCTTACACAGCTTCTCTTCTTCCCTCCGCGCTCGTCTCCCTGCTGCCCGC  
CCAGCCCTCACCCAGTGCCTCTTCTTACCGAGCTCAGAAGCCAGACTGGGAGCCCA  
CCTACAGAGGGGCAATTGACAGACTGGAGTTGAAGGCGGACGAAACGACCGCGCAGGTCA  
ATAATTCAATAAAAAAGTTAGCAACTTCTCTGTAACTTGGGTTTCAATAATTATGAGTTT  
TATGAAAACTTGAATAATAAAAAAGAAAAAATAAAAAAATAAAAAAATAAAAAA

## **FIGURE 30**

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSLVSGSATGCPFRCECSAQDRAVLCHRKCF  
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHELEELELNENIVSAVEPGAFNNLNLRLTL  
GLRSNRLKLIPLGVFTGLSNLTQDISENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRA  
FSGLSNLEQLTLEKCNLTISIPTAALSHLHGLIVRLRLHNLINAIIRDYSFKRLYRLKVLEISH  
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLA VRHLVYLRFLNLSYNPISTIEGSMHLHEL  
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTITLESVFHSVGNLETILIDSNPLA  
CDCRLLWVFRRRWRLNPNRQOPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV  
FVDEGHTVQFVCRADGDPPPAIWLSPRKHLSAKSNGRLTVFPDGTLEVRYAQVQDNGTYL  
CIAANAGGNDSPMAHLHVRYSYSPDWPHQPNKTPAFISNQPGEGEANSTRATVPFPFDIKTLII  
IATTMGFISFLGVVLFCLVLVLLFLWSRGGKNTKHNIEIYVPRKSDAGISSADAPRKFNMKMI

### **Signal sequence:**

amino acids 1-41

### **Transmembrane domain:**

amino acids 556-578

### **N-glycosylation site.**

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,  
492-496, 505-509, 526-530, 542-546

### **Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,  
607-611

### **Tyrosine kinase phosphorylation site.**

amino acids 590-598

### **N-myristoylation site.**

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,  
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

## FIGURE 31

CCCACGCGTCCGCACCTCGGCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTCGGTCAAC  
ATCGTAGTCCACCCCCCTCCCATCCCCAGCCCCGGGGATTAGGCTCGCCAGCGCCAGCC  
AGGGAGCCGGCCGGGAAGCGCGATGGGGGGCCCCAGCCGCTCGTCTCTGCTCTGCTCTGCT  
TGTTTCGCTGCTGCTGGGCGCCCGCGGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGG  
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGTCTCAAGTGCCAAAGTAAAGATCA  
CGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA  
GAGCCCTTCGAGATAATCGAATTGAGCTGGTTACCTCTACGCCCCAGGAGCTCAGCATCAGC  
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT  
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCACAGAAGCCCATCATCACTGGTT  
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCCCTAAACTGTCACTCTTCTGGGAGCAAG  
CCTGCAGCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCAT  
ACAGGAAGATCCCAATGGTAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC  
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC  
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC  
TCCCCATCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC  
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT  
GCCCTGATCTTCCCTTTCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG  
CAACATGGGCAGCTACAAGGCCCTACTACACCCTCAATGTTAATGACCCAGTCCGGTGCCCT  
CCTCTCCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCTGCTG  
CTCATCATGCTCATCTTCTTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA  
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG  
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTCATCTAGAGGCGCCTGCCCACTTCTGCTG  
GCCCCCAGGGGCCCTGTGGGGACTGCTGGGGCCGTACCAACCCGAGCTTGTACAGAGCAA  
CCGAGGGCCGCCCCCTCCGCTTGCTCCCCAGCCACCCACCCCTGTACAGAATGTCTGC  
TTTGGGTGCGGTTTGTACTCGTTTGGAATGGGGAGGGAGGAGGGCGGGGGAGGGGAGGG  
TTGCCCTCAGCCCTTTCGTTGGCTTCTCTGCATTGGGTTATTATTATTTTGTAAACATCC  
CAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA  
AACAAAAACA

## **FIGURE 32**

MGAPAASLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVVKCQVKDHEDSSLQW  
SNPAQQTLYFGEKRALRDNRILVTSTPHELISISNVALADEGEYTCSEFTMPVRTAKSLV  
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK  
TFTVSSSVTFQVTRREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ  
KLLHLHCEGRGNPVPQQYLWEKEGSPPLKMTQESALIFPPLNKSDSGTYGCTATSNMGSYKA  
YYTLNVNDPSPVPSSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLRHKGYTLTHEAKGSDD  
APDADTAIINAEGGQSGGDDKKEYFI

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 331-352

### **N-glycosylation site.**

amino acids 25-29, 290-294

### **Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

### **N-myristoylation site.**

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18



[illegible]

GGGGGTTAGGGAGGAAGGAATCCACCCACCACCCCAACCCCTTTCTCTCTCTCTCTGG  
CTCTCGGACATGGAGCACTAAATGAATCTGAATCTGTGCTGTGGCGAGACAGATGGTCTGCT  
TTACTTTGTGATGAGATCGGGGATGAATTCGCTCGCTTTAAAAATCTGCTGTTTGGATTTCTGTT  
GCTGGAGACGCTCTTTGTTTGGCCGCTGGAACGTTACAGGGGACGTTTGCAAGAGAGA  
TCTGTTTCCTGCAATGAGATAGACAGGGGACCTACAGTAGACTGTGAAAAAAGGGCTTCACA  
AGTCTGCGAGCGTTTCACTGCCCCGACTTCCCAGTTTTACCATTATTTTCTGCATGGCAATTC  
CCTCACTGCAGTTTTTCCCTAATGAGTTCGCTAAGCTTTTATAATGCGGTTAGTTTGCAACATGG  
AAAACAATGGCTTGCATGAATCGTTTCGGGGCTTTTCTGGGGCTGCAGCTGGTGCAAAAG  
CTGCACATCAACAACAACAGATCAAGTCTTTTCAAGAACGAGACTTTTCTGGGGCTGAGCG  
TCTGGAATATCTCCAGGCTGATTTTAAATTTATTACGAGATATAGACCCGGGGCTTCCAGG  
ACTTGAACAAGCTTGGAGGTGCTCAATTTTAAATGACAACTCATCAGACACCTACTGCGCAAC  
GTGTTCTCAGTATGTGCCATACACCACTGCACTCGGCTCGGGTACACAGGCTGAAAACGCTGCC  
CTATGAGGAGGCTCTGGAGCAAACTCCGTGTAATTGCGAGATCTCTGATAGGATAAACCTTT  
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGAAAACATTTCCCAAGAATGCC  
CTGATCGGGCCAGTGGTCTCGGAAGCCCCACAGAGCTGCGAGGTAAAGACCTCAATGAAC  
CACCGAACAGGACTTGTGCTCTTGAAAAACCGATGGATTAGTTAGTCTCCGGGCCCTTG  
CCCAAGACGAGACCTTTGCTCTGGAACCCCTGCCAACTCTCTTCAAGACAATGGGCAAGAG  
GATCATGGCCACACCGGGTCTGCTCCAAACGGAGGTACAAAGATCCAGGCAACTGGCAGAT  
CAAAATCAGACCCACAGCAGCATAGCGAGGTAGCTCCAGGAACAACCCTTAGCTAACA  
GTTTACCTGCCCTGGGGGCTGCACTGCGACACACATCCCAAGGCTGGGTTTAAAGATGAAC  
TGCAACAACAGGAACGTGAGACAGTCTGGTGATTGTGAAGCCAAAGCTCTCAACGTGCGAGA  
GCTTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTTGTGGATTACAAGA  
ACCTCATTTCTGTTGGATTGCGGCAACAATAACATCGCTATCTAGAGAACAACACTTCAAG  
AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACTGGACAAGCTGTCCCGGGA  
GAAATTCGCGGGGCTGAAAACCTAGAGTACTGAAACGTGGAATTAACACGCTATCCAGCTCA  
TCTTCCCGGGCACTTTCAATGCCATGGCCAAACAGGAGTCTCAATCTCAACAACAACTG  
CTGAGGTCCCTGCTGTGGAGGTGTTGCTGTGGGCTCTGCTCTCTAAACTCAGCTGTCACAA  
CAATTACTTCACTGATACCTCCGGTGCGCAGGGGTGCGTGAACAGTTAACTCCCATCAACAGA  
TAGACTCTCAGGAACCCCTGGGAGTGTCTGTCACAAATTGTGCTTTCAAGCAGTGGGCA  
GAACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCGCGGTGAACTTCTT  
TGAAAGGATTTCATGCTCTCTCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT  
CGCCACAGTTAACTTCGCACAGTAAAAACAGAGATGGGTTGGCGAGACCGGACAGCACTCC  
AACTCCTACCTAGACACCGCAGGGTGTCACTCTGGTGTGGTCCCGGGACTGCTGTGGT  
GTTTGTCACTCGCCTTACCGTGGTGGGCACTGTGTTTATTCTAGGAACAAGAAAG  
GGTCCAAGAGACGAGATGCCAACTCCTCCGCGTCCGAGATTAAATCCCTACAGACAGTCTGT  
GACTCTTCTCATGGCAATAAGGGCTTACAAACGAGACTGGGCGCCACAGAGTGTATGACTG  
TGGCTCTCACTGCTCTCAGACTAAGACCCCAACCCCAATAGGGGAGGGGACAGGGAAGGCG  
ATACATCCTTCCCAACGCGAGGCACCCGGGGGCTGAGGGGCGTGTACCAAAATCCCGCG  
CCATCAGCCTGGATGGGCATAAGTAGATAATAAAGTGTGAGCTCGCAACCTGCAAGAGGGCT  
GACCCCTTACTTAGCTCCTCTCTGAACAACAAGACGAGACTGTGGAAGCTGGGAGAGCGCA  
GCCAGCTGCTCTTTGCTGAGAGCCCCCTTTGACAGAAAGCCGACAGCCGCTGTGGAAG  
AACTGACAGTGCCTCCTGCCCTCGGCCCGGGGCTGTGGGTTGGATGCGCGGCTTCTATAC  
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTTCCCTGTGGATTAG  
CCCGTGTAGTGGCTCCTGTGTTGCTGACGAGGATGGGCAAGTGCACGAAGGCATGAATGTAT  
TGTAATAAGTATGTTTGACTTGCAC

## **FIGURE 34**

MLLWILLLETSLCFAAGNVTGDVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH  
LFLHGNSLTRLPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNKKISFRKQ  
TFLGLDDLEYLQADFNLLRDIDPGAFODLNKLEVLILNDNLISTLPANVFQYVPITHLDLRG  
NRLKTLPEYEEVLEQIPGIAEILLEDNPNWDCTCDLLSLKWELENIPKNALIGRVVCEAPTRLQ  
GKDLNETTEQDLCPLKNRVDSSLPAPPAQEETFAPGGLPTPFKTNQGQEDHATPGSAPNGGTK  
IPGNWQIKIRPTAAIATGSSRNKPLANSPLCPGGCSCDHIPGSGLKMMCNRRNVSSLADLKP  
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNY  
LDTLSREKFAGLQNLLEYLNVYNAIQILPGTFNAMEPKLRILILNNNLLRSLPVDVFAGVSL  
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGPNWECSCCTIVPFKQWAERLGSEVLMSDLKC  
ETPVNFFRKDFMLLSNDEICPOLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL  
VPGLLLVFVTSAPTVMGLVFI LRNRKRKRDRANDSSASEINSLQTVCDSSYWHNGPYNADG  
AHRVYDCGSHSLSD

### **Signal sequence:**

amino acids 1-15

### **Transmembrane domain:**

amino acids 618-638

### **N-glycosylation site.**

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 122-126, 646-650

### **Casein kinase II phosphorylation site.**

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,  
608-612, 657-661, 666-670, 693-697

### **N-myristoylation site.**

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,  
354-360, 465-471, 493-499, 598-604, 603-609

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

[illegible]

AGTGCAGCTGCGTCCCGTGTACCCGGCGCCAGCTGTGTTCCTGACCCCAAGAAATAACTCAGGGC  
TGACCCGGGGCTGGCAGCGCTCCGCACACATTTCTGTCTCGCGGGCTAAGGGAAGAACTGTGGC  
CGCTGGGGCGCGGGGGGATTCTTGGCAGTTTGGGGGTCCTGCGGAGCGAGGGCGGAGGGG  
AAGGGAGGGGGAAACCGGGTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC  
AGCTCTGCGTCTCTGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTCTCGGGGGCTCAG  
AGAATGAGGGCGGGCGTCTGCCTGTGCTCTCTTGGCAGGCGCTCTGCGCCGGGCGGGCGG  
CGCGGAAACACCCCACTGCCAGCGTGTGCTGTCTGCGGCTCGGGGGCTGCTACAGCCTG  
ACCACGCTACCATTGAAGCGCAGGCGGGCGGAGAGGCTGTCATCTGCGAGGTGGGCGCTC  
AGCACCGTTCGCTGCGGGCGCGCAGCTGCGCGCTGTGCTCTGCGCTCTCTGCGGGCAGGCCAGG  
CGCCGGAGGGGGCTCCAAAGAGCTCTGTCTTCTGGTGCAGCTGGAGCGAGCGGCTTCCCACT  
GCACCTTGAGAAACAGCACTTTGCGGGGTTTCTCTCGGCTGTCTCTCCAGCCCGCGGCTCTC  
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCTCTGCACCGCGCGGAGATGCGC  
GGTACTCCAGGCCACCGGTGGGGTGCAGCGCCGAGCGCTGGAAGAGGATGCGATGCCACTGCG  
CGCCAAACGGCTACTGTGTGACAGTCCAGTTTGGGTTTGGTGTCTGTGCTGCGCGCGCGCCGG  
GCGGCTCTTAACTTGAGCTATCGCGGCCCTTCAGCTGCACAGCGCGCTCTTGAGACTTCAG  
TCCCACTGGGACCGAGGTGAGTGCCTCTGCGGGGACAGCTCCCCGATCTGACTTACTTGCA  
TCGCGGAGCAAAATCGGCGCTCGCTGGGACAAACTCTCGGCGATGTGTTGTGCTCTGCCCC  
GGGAGGTACTTCGCTGTGGCAAATGCGCAGAGCTCCCTAACTGCCATAGACAGCTTGGGAGG  
CTTTGCGCTCGAATGTGCTACGGCTCTGCAGCTGGGGAAGGACGGCGCTCTGTGTGACCA  
GTGGGGGAAGGACAGCCGACCTTTGGGGGAGCGGGGTGCCACCAGGCGCCCGCGGCCACT  
GCAACACCGCCCGTGCAGCAGAAACATGCCCAATCAGGCTGCAGAGAAGCTGGGAGAGAC  
ACCATTGTGCCCTGAACAAAGCAATTCAGTAACTATTCTTGATAGTCTCTGATGGGAT  
CACAGAGCAGGATGTCTACCTTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTTACACC  
CATCAGGAGGCGGATTTCAAAGTTTAATTTACAGACTCTCTCTGCCACTCTCTCAGCTTT  
CGACTCTCTCTGCGCTGGTCTTATATTGTGAGCAGCAGTAGTAGTGTGGTGATCT  
TGACCATGACAGTACTGGGGCTTGTCAAGCTCTGCTTTCACGAAAGCCCTCTCTCCAGCCA  
AGGAAGGAGCTATGGGCGCGCGGGCTGGAGAGTGATCTGAGCCCGCTGCTTTGGGCTC  
CAGTTCTGCACATTGCACAAACAATGGGGTGAAGTGGGGACTGTGATCTGCGGGACAGAG  
CAGAGGGTGCTTGTCTGGCGGAGTCCCTCTTGCTCTAGTAGTGCATACCGGAAACAGGGGA  
CATGGGCACTCTGTGAACAGTTTTCACTTTGTAGTGAACCGGGAACAGAGGAACCTTAC  
TTGTGTAATGCACAAATCTCTCGAGAAATCCCTTTTCTCTAAATTCCTTTACTCCACTGAG  
GGGTAAATCAGAATGCACATCTCTCTCCCTGATGATAGAGGAAGTGAAGTGATCTTTAGA  
TAGGTACTCTGGGGGACGGGTAGTCTCTGGGGAGAGATATTTCTTAGTGTCTTCCGAGAA  
TTTGGAGAAGTGATTGAACTTTTCAGACATTGGAACAAATAGAACACAATATAATTTACA  
TTAAATAATAATTTCTGACAAATGGAAGGAAGATGTCTAATGTGTTGAGGTAGGAGTAT  
ATTGGTTCGAATTTCCAGGGGAAAAAATAAAAAATAAAATTAAGAGTTTGGTAT

## **FIGURE 36**

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS  
TVRAGAE LRAVLALLRAGPGPGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLE  
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLC PAPRPGA  
ASNL SYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIAD EIGARWDKLSGDVLCPCPG  
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSSEGQPTLGGTGVPTRRPPATA  
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVT SIPEIPRWGSQSTMSTLQMSLQAESKATITP  
SGSVISKFNSTTSSATPQAFDSSSAVVFI FVSTAVVVLVILTMTVLGLVKLCFHESPSSQPR  
KESMGPPGLSEDP EPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 399-418

### **N-glycosylation site.**

amino acids 189-193, 381-385

### **Glycosaminoglycan attachment site.**

amino acids 289-293

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 98-102, 434-438

### **Casein kinase II phosphorylation site.**

amino acids 275-279, 288-292, 342-346, 445-449

### **N-myristoylation site.**

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

## FIGURE 37

CGGACGCGTGGGATTAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG  
CGTCGAGTCAGACGGCACCATATCGCCTTTAAAGTGCCTCCGCCCTGCCGGCCGCGTATC  
CCCCGGCTACCTGGGCGGCCCGCGCGCGGTGCGCGCTGAGAGGGAGCGCGCGGGCAGCCGA  
GCGCGCGTGTAGCCAGCGCTGCTGCCAGTGTGAGCGCGCGGTGTGAGCGCGGTGGTGCGGA  
GGGGCGTGTGTGCCGGCGCGCGCGCGTGGGGTGCAAACCCCGAGCGTCTAGCCTGCCATGA  
GGGGCGCGAAGCGCTGGGGCGCCACTCTGCCTGCTGCTGGCTGCCGCCACCCAGCTCTCGCGG  
CAGCAGTCCCCAGAGAGACCTGTTTTCACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT  
TATTGGCAGTGAAGGTTTCTCTGGAGTGTACCCTCCAAATAGCAAATGTACTTGGAAATTA  
CAGTTCCCGAAGGAAAGTAGTCGTTCTCAATTTCCGATTATAGACCTCGAGAGTGACAAC  
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTGGCCG  
CTTCTGTGGCACTTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA  
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA  
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCCGGCTCTTTTAAAC  
CCCCAACTGGCCAGACCGGATTACCTTGCAGGAGTCACTTGTGTGTGGCACATTGTAGCCC  
CAAAGAATCAGCTTATAGAATTAAGATTTGAGAAGTTTGATGTGGAGCGGAGATAACTACTGC  
CGATATGATTATGTGGCTGTGTTTAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGGAAA  
GTATTGTGGTATAGTCCACCTGCGCCAATTGTGTCTGAGAGAATGAACCTCTTATTAGT  
TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTATGTGTCACTACATATTCAGGCCAAAA  
AAACTGCCATACAACCTACAGAACAGCCTGTCAACACCACTTCCCTGTAACACGGGTTTAAA  
ACCCACCGTGGCCTTGTGTCAACAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT  
GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCAACACCATCACTCGCGATGGGAGTTTG  
CAGCCACAGTCTCGATCATCAACATCTACAAGAGGGAAATTTGGCGATTTCAGCAGGCGGG  
CAAGAACATGAGTGCCAGGCTGACTGTGCTGTGCAAGCAGTGCCTCTCTCAGAAAGAGTCT  
TAAATTACATTTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCAAAATCATGCCAACAGC  
TTTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAATAAGCAATG  
TTAAAGTGAAGTGTGTCCATTTAAGCTGATTTCTGCCATTGCCTTTGAAAGATCTATGTTT  
TCTCAGTAGAAAAAAATACTTATAAAATTACATATTTGAAAAGAGGATTCGAAAGATGG  
GACTGGTTGACTCTTTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAGTCTT  
TGCTGTGTGAGAGGAGCAGCTATCTGATTGGAAACCTGCCGACTTAGTGCGGTGATAGGA  
AGCTAAAAGTGTCAAGCGTTGACAGCTTGAAGCGTTTATTATACATCTCTGTAAAAGGAT  
ATTTTAGAATTTAGTTGTGTGAAGATGTCAAAAAAGATTTTAGAAGTGCAATATTATAGT  
GTTATTTGTTTCACTTCAAGCCTTTGCCCTGAGGTGTTACAATCTTGTCTTGCCTTTCTA  
AATCAATGCTTAATAAAATATTTTAAAGGAAAAA

CGGACGCGTGGGATTAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG

## **FIGURE 38**

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK  
ITVPEGKVVLNFRFIDLESDNLCRYDFVDVYNHANGQRIGRFCGTFRPGALVSSGNKMMV  
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV  
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPPAPIVSERNELLI  
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTTFPVTTGLKPTVALCQCKRRTGTLEGN  
YCSSDFVLAGTVITITITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLR  
GLNYIIMQVGEDGRGKIMPNSFIMPFKTKNQKLLDALKNQC

### **Signal sequence:**

amino acids 1-23

### **N-glycosylation site.**

amino acids 355-359

### **Casein kinase II phosphorylation site.**

amino acids 64-68, 142-146, 274-278

### **Tyrosine kinase phosphorylation site.**

amino acids 199-208

### **N-myristoylation site.**

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,  
305-311, 309-315, 320-326, 330-336

### **Cell attachment sequence.**

amino acids 149-152

## FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCGCGGGCTGGGGCGGTTCGCTTCTT  
CCTTCTCCGTGGCCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCATGGCCCCGAAGG  
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCTCAACCTCCCAGGACCTATCTGG  
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCTCAGCCCCATCCGTGTATACCTG  
CCGGGGACTGGTTGACAGCTTTAAACAAGGGCCTGGAGAGAACCATCCGGGACAACTTTGGAG  
GTGGAACACTGCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCCTG  
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT  
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTCAACAAGCAGCAGGAGGGCCCCGGACCTCTTCC  
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTTCGGGCCCTCCTGC  
CTTCCCTGTCTGGGGGAACAGAGAGGGCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG  
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCC  
AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGT  
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAAGTGTTCGAATGCAAGAAGGG  
CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACT  
GTGGAGCTGACCAATTTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG  
GCCTGCCTAGGCTGCATGGGGGCAGGGCCAGGTCGCTGTAAGAAGTGTAGCCCTGGCTATCA  
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA  
ACAAGCAGTGTGAAAACACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG  
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC  
AGAAGACGAGTTGGTGGTGTCTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGEC  
CGCTGGCTGCTAAGGGCGACTTGGTGTTACCGCCATCTTCATTGGGGTGTGGCGGCCATG  
ACTGGCTACTGGTTGTGAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA  
ATCGCGGCCACACCTGTAGGACCTCCTCCACCCACGCTGCCCCAGAGCTTGGGCTGCC  
TCCTGCTGACACTCAGGACAGCTTGGTTATTTTGTGAGAGTGGGGTAAGCACCCCTACCTG  
CCTTACAGAGCAGCCCAGGTACCCAGGCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGC  
CCTGAAGGTGGATACCATGAGCTCTTCACTGGCGGGACTGGCAGGCTTCACAATGTGTGA  
ATTTCAAAGTTTTCCTTAATGGTGGCTGCTAGAGCTTTGGCCCTGCTTAGGATTAGGTG  
GTCTCACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGTGCATGTGCCAGTTCTCTGT  
TCTGTGTTACACATCCCCACACCCATTGCCACTTATTTATTATCTCAGGAAATAAAGA  
AAGGTCTTGGAAAGTTAAAAA

## **FIGURE 40**

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER  
TIRDNFGGGNTAWEENLSKYKDS ETRLVEVLEGVCSKSDFECHRLLLELSEELVESWNWFHKQ  
QEAPDLFWLCSDSLKCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDCQAG  
YGGEACGQCGLGYFEAERNASHLVCSACFGPCARCSGPEESNCLQCKKGWALHHLKCV DIDE  
CGTEGANCGADQFCVNTESGYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE  
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVV LQQMFFG  
I IICALATLAAGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGF1KGR

### **Signal sequence:**

amino acids 1-29

### **Transmembrane domain:**

amino acids 372-395

### **N-glycosylation site.**

amino acids 79-83, 205-209

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 290-294

### **Casein kinase II phosphorylation site.**

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

### **N-myristoylation site.**

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,  
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,  
326-332, 372-378, 395-401

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 321-333

### **EGF-like domain cysteine pattern signature.**

amino acids 181-193



## FIGURE 41

TGAGACCCCTCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA  
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCTTGCCAGCCCCGGG  
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCTGTGCGGCAGCTGCAGCTCAAAGAGGT  
GCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCCAGT  
ACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGCTCCCGCGGAAAGAGGTTTCAGCCAGAGC  
TTCCGAGAGGTGGCCGGCAGGTTCTTGGCGTTGGAGGCCAGCACACACCTGCTGGTGTTTCGG  
CATGGAGCAGCGGCTGCCGCCCAACAGCGAGCTGGTGCAGGCCGTGCTGCGGCTCTTCCAGG  
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGGCGGCTGTCCCCGCGCAGCGCCCCGGGCC  
CGGGTGACCGTTCGAGTGGCTGCGCGTCCGCGACGACGGCTCCAACCGCACCTCCCTCATCGA  
CTCCAGGCTGGTGTCCTCCACGAGAGCGGCTGGAAGGCCCTTCAGCGTGACCGAGGCCGTGA  
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGTGCTACAGGTGTGGTGACAGG  
GAGCATCTGGGCCCCCTGGCGTCCGGCGCCCAAGCTGGTCCGCTTTCGCTCGCAGGGGGC  
GCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCCTGACCTTGGGGACTATGGAG  
CTCAGGGCGACTGTGACCCTGAAGCACCATGACCGAGGGCACCCGCTGTGCCGCCAGGAG  
ATGTACATTGACCTGCAGGGGATGAAGTGGGCCGAGAACTGGTGCTGGAGCCCCGGGCTT  
CCTGGCTTATGAGTGTGTGGGCACCTGCCGGCAGCCCCGGAGGCCCTGGCCTTCAAGTGGC  
CGTTTCTGGGGCCTCGACAGTGCATCGCCTCGGAGACTGACTCGCTGCCCATGATCGTCAGC  
ATCAAGGAGGGAGGCAGGACCAGGCCCCAGGTGGTCAGCCTGCCCAACATGAGGGTGCAGAA  
GTGCAGCTGTGCCTCGATGGTGCGCTCGTGCCAAGGAGGCTCCAGCCATAGCGCCTAGTG  
TAGCCATCGAGGGACTTGACTTGTGTGTGTTTCTGAAGTGTTGAGGGTACCAGGAGAGCTG  
GCGATGACTGAACCTGCTGATGGACAAATGCTCTGTGCTCTCTAGTGAGCCCTGAATTTGCTT  
CCTCTGACAAGTTACCTCACCTAATTTTGTCTCTCAGGAATGAGAATCTTTGGCCACTGGA  
GAGCCCTTGCTCAGTTTTCTCTATTCTTATTATTCACTGCACCTATATTCTAAGCACTTACAT  
GTGGAGATACTGTAACTGAGGGCAGAAAGCCANTGTGTCACTGTTTACTTGTCTGTCTCAC  
TGGATCTGGGCTAAAGTCTCCACCACCACTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT  
TGTGCATCCCCAATCCAGATAATAAAGACTTTGTAAACATGAATAAACACATTTTATTCT  
AAAA

## **FIGURE 42**

MQPLWLCWALWVPLASPGAALTGEQLLGSLRLRQLQLKEVPTLDRADMEELVIPTHVRAQYV  
ALLQRSHGDRSRGKRFSQSFREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP  
VPKAAALHRHGRLSPRSARARVTVEWLVRDDGSNRTSLIDSRLVSVHESGWKAFDVTAVNF  
WQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLDGYGAQ  
GDGCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCTCRQPEALAFKWWF  
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVS LPMNRVQKCSASCASDGALVPRRLQP

### **Signal sequence:**

amino acids 1-18

### **N-glycosylation site.**

amino acids 158-162

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 76-80

### **Casein kinase II phosphorylation site.**

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

### **N-myristoylation site.**

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

### **Amidation site.**

amino acids 74-78

### **TGF-beta family signature.**

amino acids 282-298

## FIGURE 43

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTGTCAGTGGCCTGATCGCGATGGGGACAAA  
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG  
CATTGGGCAGTGTTACAGTGCACCTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT  
GTGAAGTTGTCTGTGCCTACTCGGCTTTTTCTTCTCCCGTGTGGAGTGGAAGTTTGACCA  
AGGAGACACCACCAGACTCGTTTGTCTATAATAACAAGATCAGACTTCTCTATGAGGACCGGG  
TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC  
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT  
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCTCTCTGCCACCATTGGGAACCGGG  
CAGTGCTGACATGCTCAGAACAAAGATGGTTCCTCCACCTTCTGAATACACCTGGTTCAAAGAT  
GGGATAGTGATGCCTACGAATCCCAAAAGCACCCGTGCCTTCAGCAACTCTTCTCTATGTCCT  
GAATCCCAACAACAGGAGAGCTGGTCTTTGATCCCTGTGAGCCTCTGATACTGGAGAATACA  
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT  
GTGGAGCGGAATGTGGGGGTCTCGTGGCAGCCGCTCTTGAACCTGATTCTCCTGGGAAT  
CTTGGTTTTTGGCATCTGGTTTGCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGA  
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG  
ACCTCGTCATTCTCTGGTGTGAGCCTGGTCGGCTCACCGCCTATCATCTGCATTTGCCTTACT  
CAGGTGCTACCGACTCTGGCCCCCTGATGTCTGTAGTTTCACAGGATGCCTTATTTGTCTTC  
TACACCCCAAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC  
ATCCTCCTTCATGCCCTCCCTCCCTTTCCTACCACTGCTGAGTGGCCTGGAACCTGTTTAAA  
GTGTTTATTCCTCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC  
TTCTAAGTAGACAGCAAAAATGGCGGGGTGCGAGGAATCTGCACTCAACTGCCACCTGGC  
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTCTGGGCTCTTCCCTGTGTACTGAC  
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTGTGTTGG  
TGATGACACTGGGGTCCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG  
CCACTGGGATCCCTCTGCCCTGTCTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGT  
GGAAAATGGGAGCTCTTGTGTGGAGAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAG  
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTG  
TAATCCAGAGGCTGAGGCAGGCGGATCACTGAGTTCGGAGTTCGGGATCAGCCTGACCA  
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGATGCCTGTGTAGTC  
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAA

## **FIGURE 44**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEW  
KFDQGDTTRLVCYNNKITASYEDRVTFLEPTGITFKSVTREDTGTYYTCMVSEEGGNSYGEVKV  
KLIVLVPPSKPTVNIPISSATIGNRAVLTCSEQDGSPPEYTWFKDGIVMPTNPKSTRAFSNS  
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTTPMTSNAVRMEAVERNVGVIVA AVLVTLI  
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

### **Signal sequence:**

amino acids 1-27

### **Transmembrane domain:**

amino acids 238-255

### **N-glycosylation site.**

amino acids 185-189

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

### **Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

### **N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

## FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGACGGCGGTTGGATGGCGCAGGTTGGA  
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT  
GGAGGCCGCGCGAGCCCGCTTTCCACCCGACCTCTGCCCAGGCCGAGGCCCCAGCTCAG  
GCTCGTGCCCAACCACCAAGTTCAGTGCCGCACAGTGCGCTTATGCGTGCCCCCTCACCTGG  
CGCTGCGACAGGACTTGACTGTCAGCGATGGCAGCGATGAGGAGGAGTGACGATTGAGCC  
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCCTGCCCTGCACCGCGTCA  
GTGACTGCTCTGGGGGAACAGACAAGAACTGCGCAACTGCAGCCGCCTGGCCTGCCTAGCA  
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA  
CCCAGACTGTCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGAAG  
GGGATGCCACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCACCTCTCTCAGGAATGCC  
ACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCTCTGTGCGGAATGCCACATCCTC  
CTCTGCGGAGACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCAGCTGTGCGGTGC  
TCAGTGCAAGCCTGGTCAACGCCACCCTCCTCCTTTGTCTGGCTCCGAGCCCAGGAGCGC  
CTCCGCCCACTGGGGTTACTGGTGCCATGAAGGAGTCCCTGCTGCTGTGAGAACAGAAGAC  
CTCGTGCCCCTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACA  
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT  
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAAGTGCCCTGGAGATTGAGGGTCCC  
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAAGTGA  
GGGCTGGCCCAGGCAGCTCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG  
CCCCGTCTGAGGTTGGCGATTAAAGTTGCTTC

## **FIGURE 46**

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR  
TSGLCVPLTWRCRDLDCSDGSDEEECRIEPCTQKGQCPCPPPGPLPCPCTGVSDCSGGTDKKL  
RNC SRLACLAGE LRCTLSDDCIPLTWRC DGHPCPDSSDELGCGTNEILPEGDATTMGFPVT  
LESVTS LRNATTMGFPVTLESVPSVGNATSSSAGDQSGSP TAYGVIAAAVLSASLVTATLL  
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTS LP

### **Signal sequence:**

amino acids 1-30

### **Transmembrane domain:**

amino acids 230-246

### **N-glycosylation site.**

amino acids 126-130, 195-199, 213-217

### **Casein kinase II phosphorylation site.**

amino acids 84-88, 140-144, 161-165, 218-222

### **N-myristoylation site.**

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,  
224-230, 230-236, 263-269

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 44-55

### **Leucine zipper pattern.**

amino acids 17-39

## FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTCGCGCACAGATGCGG  
GTTAGACTGGCGGGGGGAGGAGGCGGAGGAGGGAAGGAAGTCATGCATGAGACCCACAGA  
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG  
GAGATGGATTCTTAGAGCAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG  
GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT  
CGATGACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG  
GAGGGGTTTTCTTGAAGGCTCTGTAGCCCGATTTCACTGCCAAGACGGAATTCAGCTGAAG  
GGCGCTACAAAGAGACTGTGTTTGAAGCATTTTAATGGAACCCTAGGCTGGATCCCAAGTGA  
TAATTCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTATA  
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTATGAAGGATTCAGATCCGG  
TACCCCGACCTACACAAATATGGTTTCATTATGTCGCGATGATGGAACGTGGAATAATCTGCC  
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC  
TCCAGACCTCCTTCCGGGTGGGACTGTGATCTCCTATCGCTGCTTTCGCGATTTAAACTT  
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCACCCCGGTG  
CCTTGCTCTGGAAGCCCAAGCTGTGCCACTACCTCCAATGGTGAGTCACGGAGATTTTCGTCT  
GCCACCCGCGGCCTTGTGAGCGCTACAACCACGGAAGTGTGGTGGAGTTTTACTGCGATCCT  
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCTTCT  
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCACGACCCATGAGACCCCTCTGA  
CCACGTGGAAGATTGTGGCGTTACGGCAACCAAGTGTGCTGCTGCTGCTGCTCGTCATC  
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTTCCCCCAGGGGGCCTCCCCGGAG  
TTCAGCAGTGACCCTGACTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCTATG  
ACGAAGCTGTGAGTGGCGGCTTGAAGTGCCTTAGGCCCCGGGTACATGGCCTCTGTGGGCCAG  
GGCTGCCCTTATCCCGTGGACGACACAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGA  
CACAGGCCACAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAA  
GTCTGTATTACCTCCCAGGTGCCAAGAGAGCACCCACCCTGCTTCGGACAACCTGACATA  
ATTGCCAGCAGGCAGAGGAGGTGGCATCCACAGCCAGGCATCCATCATGCCCACTGGGT  
GTTGTTCTTAAGAACTGATTGATTAAAAAATTTCCCAAAGTGCCTGAAGTGTCTCTTCAA  
ATACCTGTTGATCTGTGAGTTGATTCCCTTCCCTTCTCTTGTTTTAGACAAATGTAAACAA  
AGCTCTGATCCTTAAATGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC  
CTGTTTCTTCTTGACACAGACTGATTAAAAATTAAGNAAAAA

## **FIGURE 48**

MYHGMNPSNGDGFLEQQQQQQQSPQRL LAVILWFQLALCFGPAQLTGGFDDLQVCADPGI  
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHPNGTLGWIPSDNSICVQEDCRI  
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS  
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP  
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT  
WPSTHETLLTTWKIVAFATATSVLLVLLLVILARMFQTKFAHFPPRGP RSRSSSDPDFVVVD  
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD TDTGPGESETCDS  
VSGSSELLQSLYSPPRCQESTHPASDNPDI IASTAEVASTSPGIHHAHWVFLRN

### **Signal sequence:**

amino acids 1-41

### **Transmembrane domain:**

amino acids 325-344

### **N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

### **Casein kinase II phosphorylation site.**

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472

### **N-myristoylation site.**

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405



## FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGC GGTCCGTCCGTGGCCTAGAGA  
TGCTGCTGCCGCGGTTGCAGTTGTTCGCGCAGCCTCTGCCCGCCAGCCCGCTCCACGCGCGT  
AGCGCCCGAGTGTCGGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGGAACCGCGCTACAGG  
CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCC  
TCGGAATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCCTTGTTA  
TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACCTTGAGGAAGCCAAAGAAGCCT  
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA  
AAGTTCATTGAAAACTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA  
GGAGAAACAAAGCAATAGCAGAGCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATAT  
CACAAATTTAGGAACTGGTATGTGGATGAGCCGCTCTGCGGCAGCGAGGTCTGCGTGGTCA TG  
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTTACATGTTCCAGTGGAAATGATGA  
CCGGTGCAACATGAAGAACAAATTTCAATTTGCAAAATATTCTGATGAGAAACCAGCAGTTCCCTT  
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAAACCTGTACTTCCAGAAGAAACACAG  
GAAGAAGATGCCAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCACAT  
CCTAATCCCCAGCATTCCCCCTTCTCCTCCTCCTTGTGGTCAACACAGTTGTATGTTGGGTTT  
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCTAGCACAAAGAAGCAACACACCATC  
TGGCCCTCTCCTCACCAGGGAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA  
AAGCGAAGCTGACTTAGCTGAGACCCGCCAGACCTGAAGAATATTTCAATCCGAGTGTGTT  
CGGGAGAAGCCACTCCCGATGACATGCTTGTGACTATGACAAACATGGCTGTGAACCCATCA  
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGGAGAGTGGATTTGTGACCAATGACATTTATGA  
GTTCTCCCAGACCAAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAATGAAATATATG  
GTTATTAGGACATATAAAAACTGAACTGACAACAATGGAAGAAAGAAATGATAAGCAAAATC  
CTCTTATTTTCTATAAGGAAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCTCTGT  
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTTGGCTGTATCCTTTAT  
CCCAGCCAGTATCCAGCTCGACCTTATGAGAAGGTACCTTGCCAGGTCTGGCACATAGTA  
GAGTCTCAATAAATGTCACTTGGTTGGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTG  
GCAGTGATAAGATGGGCTGTGGAGCTTGGAAAACACCTCTGTTTTCTTGCTCTATACAG  
CAGCACATATTATCATACAGACAGAAAATCCAGAATCTTTTCAAAGCCCACATATGGTAGCACAG  
GTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTTTCAAAGAATAAAATCAAATAAAGA  
GCAGGAAAAAAA

## **FIGURE 50**

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSRRL  
NFEEAKEACRRDGGQLVSI ESEDEQKLEKFIENLLPSDGD F WIGLR RREEKQSNSTACQDL  
YAWTDGSI SQFRN WYVDEP SCGSEVCVVMYHQPSAPAGIGGPYMFQWNDRCNMKNNFICKY  
SDEKPAVPSREAEGETELTTPVLPEETQEEDAKKTFKESREAA NLAYILIPSIPLLLLLLV  
VTTVVCWWVICRKRKRQPDPTKKQHTIWSPHQGNSPDLEVYNVIRKQSEADLAETR PDL  
KNISFRVCSGEATPDDMSCDYDNMAVNPSES GFVTLVSVESG FVTNDIYEFSPDQMGRSKES  
GWVENEIYGY

### **Signal sequence:**

amino acids 1-21

### **Transmembrane domain:**

amino acids 235-254

### **N-glycosylation site.**

amino acids 117-121, 312-316

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 296-300

### **Casein kinase II phosphorylation site.**

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,  
299-303, 306-310, 323-327

### **N-myristoylation site.**

amino acids 18-24, 37-43, 76-82, 146-152

## FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC  
ATCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT  
GTTTGCCCTCCTGCAACCTCAACCCGGAGGCGAGCGAGGGCCTACCACCATGATCACCTGGTGT  
GTTTCAGCATGCGCTTGTGGACCCAGTGGGCGTCCTGACCTCGTGGCGTACTGCCTGCACC  
AGCGCGGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC  
CTGCTGAAGTTGAAAAATGGTGCAGGTCTGTGTTTCGACACGGGGCTCGGAGTCTCTCAAGCC  
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCCAAACTC  
AGTTTGATTACACAGTCAACAACTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT  
CAATACCATGAGACCACCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCAT  
GCAGCAAATGTTTGCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC  
TTTCACCAACCTTCAACCCACAGGAGGTCTTTATTCGTTCCACTAACATTTTTCGGAATCTG  
GAGTCCACCCGTTGTTTGCTGGCTGGGCTTTTCCAGTGTGAGAAAGAAGGCCCATCATCAT  
CCACACTGATGAAGCAGATTGAGAAGTCTTGATCCCAACTACCAAGCTGCTGGAGCCTGA  
GGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTG  
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCTCTCT  
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCATGCTGAAGAGATTTG  
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGTACATACTGCCCAAGGAAGACAGG  
GAAAGTCTTCAGATGGCAGTAGGCCCATCTCTCCACATCTTAGAGAGCAACCTGCTGAAAGC  
CATGGACTCTGCCACTGCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG  
TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTGTACCACAAATGGCCACCGTTTGCT  
GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA  
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGT  
TCTTGAATGCCATGTGAGTTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA  
ACTCAGGTGATGGAAGTTGGAATGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATT  
TTAAAAATAAAGTGCTTTTATACAATG

## **FIGURE 52**

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLMVQVVFRHGAR  
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL  
TKVGMQQMFALGBRLRKNYVEDIPFLSPTFNPQEVFIRSNIFRNLESTRCLLAGLFCQCKE  
GPIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLLKKVKDRMGIDSSDKVD  
FFILLDNVAAEQAHNLPSCPMLKR FARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLILES  
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLMLTLGIFDHKWPPFAVDLTMELYQHLESKEW  
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMS VYTLSPEKYHALCSQTQVMEVGNEE

### **Signal sequence:**

amino acids 1-23

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

### **Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

### **Tyrosine kinase phosphorylation site.**

amino acids 280-288

### **N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

### **Amidation site.**

amino acids 216-220

### **Leucine zipper pattern.**

amino acids 10-32

### **Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

## FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT  
TAAATTTGAGCTCATCACCTTACCTGCCTTGGTCATGGCTCTGCTATTCTCCTTGATCCTT  
GCCATTTGCACCAGACCTGGATTCTTAGCGTCTCCATCTGGAGTGCGGCTGGTGGGGGGCCT  
CCACCGCTGTGAAGGGCGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG  
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC  
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCCCTCATCCA  
ATCAGTCAGTTGCACAGGAACAGAAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG  
ATTGTTACATGATGAAGATGCTGGGGCATCGTGTGAGAACCCAGAGAGCTCTTTCTCCCCA  
GTCCAGAGGGTGTCAAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAGTGAA  
GCACCAGAACCAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGCAAGGTGG  
TGTGCCGCGAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC  
TATGGCCGAAAAACCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCCTTCA  
GGATTGCCCTTCTGGGCCCTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTCTG  
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG  
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACCTGGGGAGAAAAGGAGGA  
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA  
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTGTTGCTCAGGGGAGGAG  
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTCACGACTGCACCCACCAGGAAGA  
TGTGGCTGTCATCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA  
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGGATGAACACTGATCT  
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCCTTCAGAGTTGG  
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACTACATCA  
CCACCTTTCTATGTCTCCACATTGCACACAGCAGATTCACAGCCTCCATAATTGTGTGTAT  
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACATA  
CACCATTTGTCTGTTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA  
TTCTAGAGGAACGGAATTTTAAAGGATAAATTTCTGAATTGGTTATGGGGTTTCTGAAATTG  
GCTCTATAATCTAATTAGATATAAAATCTGGTAACTTTATTTACAATAATAAGATAGCAC  
TATGTGTTCAAA

## **FIGURE 54**

MALLFSLILAICTRPGFLASPSGVRLVGGHLRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC  
RELGCGAASGTPSGIlyEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEVEYDCSHDEDAGASC  
ENPESSFSFVPEGVRLADGPGHCKGRVEVKHQNQWYTVQCQTGWSLRAAKVVCRQLGCGRAVL  
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG  
GDNLCSGRLEVLHKGWVGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL  
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

### **Signal sequence:**

amino acids 1-15

### **Casein kinase II phosphorylation site.**

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,  
267-271, 294-298, 316-320, 336-340

### **N-myristoylation site.**

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,  
180-186, 263-269, 286-292

### **Amidation site.**

amino acids 196-200

### **Speract receptor repeated domain signature.**

amino acids 29-67, 249-287

## FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCTCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC  
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCGGCTACCAGGAAGAGTCTGCCGAAG  
GTGAAGGCCATGGACTTTCATCACCTCCACAGCCATCTGTCCCTGCTGTTTCGGCTGCCTGGG  
CGTCTTCGGCTCTTCCGGTGTCTGCAGTGGGTGCGCGGGAAGGCCTACCTGCGGAATGCTG  
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAAGTCTTCTATGCT  
GCGGTGTCTAAACTGGTGTCTGTGGCCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA  
ACTTACCGCTTCTCATGCCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC  
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC  
GACATACTTGTCACAATGTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA  
TGTGGACAAGAGGGTTCATGGAGACAACTACTTTGGCCAGTTGCTCTAACGAAAGCACTCC  
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTGCCATCAGCAGCATCCAGGGCAAG  
ATGAGCATTCTCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTTGA  
CTGTCTGCGTCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCGGCTACA  
TCCACACCAACCTCTCTGTAAATGCCATCACCGCGATGGATCTAGGTATGGAGTTATGGAC  
ACCACCACAGCCCAGGGCCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTTGCTGTGTGGG  
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCTTTGGCTGTTTATCTTCGAA  
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC  
AAGAACTCCTTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC  
TTACTCTACAAGGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTTGTCTCACAAGTGGG  
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA  
AGCTTCTTCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTAAACACT  
AAAAACTAGAAATAAACATCTCAACAGTAAAAAAAAAAAAAAAAAGGGCGGCCGCACTCTAG  
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTTTATATGCAGCTTATAATGGTTAC

## **FIGURE 56**

MDFITSTAILPLLFGLGVFGLFRLLQWVRGKAYLRNAVVTGATSGLGKECAKVFYAAGA  
KLVLCGRNGGALBELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGYVDIL  
VNNAGISYRGTIMDTTVDVDRVMEETNYFGPVALTKALLPSMIKRRQGHIVAISIIQKMSI  
PFRSAYAASKHATQAFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDDTT  
AQGRSPVEVAQDVLAAGVKKKKDVILADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

### **Signal sequence:**

amino acids 1-21

### **Transmembrane domain:**

amino acids 104-120, 278-292

### **N-glycosylation site.**

amino acids 228-232

### **Glycosaminoglycan attachment site.**

amino acids 47-51

### **Casein kinase II phosphorylation site.**

amino acids 135-139, 139-143, 253-257

### **Tyrosine kinase phosphorylation site.**

amino acids 145-153, 146-153

### **N-myristoylation site.**

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

### **Amidation site.**

amino acids 265-269

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 6-17





## **FIGURE 58**

MKFLLDILLLLPLLVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAIEGDVSILVNNAGVV  
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH  
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDDAVIGYKMKQA

### **Signal sequence:**

amino acids 1-19

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34, 283-287

### **Casein kinase II phosphorylation site.**

amino acids 52-56, 95-99, 198-202, 267-271

### **N-myristoylation site.**

amino acids 43-49, 72-78, 122-128, 210-216



## **FIGURE 60**

MVGAMWKVIVSLVLLMPGCDGLFRSLYRSVSMPPKGDGSGQLFLTPYIEAGKIQKGRELSL  
VGPPFGLNMKSYAGFLT VNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH  
GPYVVTSNMTLRDRDFPWTTL SMLYIDNPFVGTGFSFTDDTHGYAVNEDDVARDLYSALI QF  
PQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSNPNPREVKINLNGIAIGDGYSDPESIIGG  
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGDLTSDPSYFQNVGT  
CSNYYNFLRCTEPEDQLYYVKFSLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT  
EIMNNYKVLIIYNGQLDIIVAAALTE RSLMGMDWKGSQYKKA EKKVWKIFKSDSEVAGYIRQ  
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYKGWDPYVG

### **Signal sequence:**

amino acids 1-22

### **N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

### **Casein kinase II phosphorylation site.**

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,  
353-357, 424-428

### **Tyrosine kinase phosphorylation site.**

amino acids 423-432

### **N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

### **Serine carboxypeptidases, serine active site.**

amino acids 200-208

### **Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTGTGGCTACAACAT  
TTTTCCCTTTCTTACAAGTTTCTAACAGCTGTGTCTAACAGCTAGTGAATCAGGGGTCTTCTT  
CTGGGAGTAAGAAGGCTTGAGGCGAGGACAGGGCACTCTACTCAGGGTGACAGCTCTCTTG  
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCACGGGAGTGAGGTGATGGAAG  
TCTAAATAGGAGAAGAAATTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGGC  
CTGGGGAGGGCTGCTTAAACAAGCTTTCAAAAAACAGGAGGCACTTCCACTGGGCTGGGAT  
AAGACGTGCGCGGTAGGATAGGGAAGACTGGGTTTGTCTTAATATCAAAATGAGCTGGGTGGT  
TGAACCTTCAACAGCCTTTTAACTCTCTGGGAGATGAAACATGAGTCTTAAGGGCCAGAAAG  
TAGAGATGCTTTGTAAAAATAAAATTTAAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA  
GCACAAAATAGATAACAAGGATTTCTCTGAACATTCTTAAGAGGAGGAAAGTATGTTAAAAATA  
GAAAAACCAAATGTCGAGAAGGAGGAGCACTCAGACGATTAACCCAGTGGGACCGCTGGGT  
AGGCGAGCCTTTTGTGCTCCTCCCGGAAATTTATTTTGGTCTGACCACTCTGCCTTTGTGTTT  
GCAGAAATCTGTGAGGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCGGTCT  
CCTCACGCGCGCCCTCTCAGACTGACAGAGCAGCGCTGGCCCGCGGCCCTGGAGGTGG  
ACAGCGCTCTGTGGTCTGTGCTCTAGAGTGTGGTGCTGTGGCCCTCCAGCAGCGCGC  
ATGCTCTCAGTCTCAGACCTTCCACTCTGAGAATTCTGACATGCACTGAACCTTCAACCAT  
CCACCAAGGACGCGGGGCCGTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA  
ACCTGACCATCAAGGTGGCTCATAAGCAGGCGCCAGAGGAGCAACAAGTTCTCGTTACC  
CCCTCATCTGTGAGCCCTGACGAGCAAGTGTCAACCTCAGCAACAATGTCACAAAGCTGCT  
CATCTTGACTACTCTGAGAACCGCCTGTGGCTGTGGGAGCCTCTACCAAGGGGTCTGCA  
AGCTGTCTCGGGCTGGATGACCTTCTATCTGTGGTGGAGCCATCCCAAGAAGGAGCACTAC  
CTGTCCAGTGTCAACAAGACGGGCAACATGATACGGGTGATTGTGCGCTCTGAGGTGAGGA  
TGGCAAGCTCTTCACTCGCAGCGGTGTGGATGGGAAGCAGGATTACTTCCGACCGCTGTCCA  
CGCGGAGCTGCCCGGACACCTGAGTCTCTCAGCATGTCTGCAATGAGCTACACAGCAT  
TTTGTCTCCTCTCTCATCAAGATCCCTTCAGACACCTTGGCCCTGGTCTCCACCTTGACAT  
CTTCTACATCTACGGCTTTGTGATGGGGGGCTTTGTCTTCTTCTCACTGTCTCAGCGCCGAGA  
CCCCTGAGGGTGTGGCCATCAACTCGGCTGTGGAGCACTCTCTACACTCAGCATCTGTGCGG  
CTCTGCAAGGATGACCCCCAGTTTCACTCATAGTGTCTCCTGGCCCTTGGGCTGCACCCGGGC  
CGGGTGGGAATACCGCTCTCTGAGCCTGTCTTACTGGCCAGCCTGGGACTCAGTGGCC  
AGGCTCTCAATATCACCAGCCAGGAGATGACTCTTTGGCATCTTCTCCAAAGGGCAGAAG  
CAGTATCACCAACCGCCGATGACTCTGCCCTGTGTGCTCTTCCATCTCGGGCCATCAACT  
GCAGATCAAGGAGCGCTGTGAGTCTGTCTACAGGGCGAGGGCAACTGGAAGCTCAACTGGC  
TGCTGGGGAAGGATCCAGTGACAGGAAGCGCCTGTCCCATCGATGATACTTCTGTGGA  
CTGGAATCAACACGCCCCGGGAGGCTCAACTCCAGTGGGAGGCTGACCTGTACACCA  
CAGCAGGACCGCATCACTCTGTGGCTCTCTAGCTTTTACAACGGCTACAGCGTGGTTTTTG  
TGGGACATAAGAGTGGCAAGCTGAAAAAGGTAAAGATCTATGAGTTCAGATGCTCCATGGC  
ATTCACCTCTCAGAAAGAGTCCCTCTGGAAGGTAGCTATTTGGTGGAGATTTAACTATG  
GCACTTTTATTTCTTGGGGAACAAAGGTGAATGGGAGGTAAGAAGGGGTTAATTTTGTG  
ACTTACCTTCTAGTACTTCTCTCAGCACTCAGTCACTATGGGTATGTAAGGAATGCAAGCGTA  
TTTCAATATTTTCCAAACTTTAAGAAAAAATTTAAGAAAGTACATCTGCTCAAAAGCA

## **FIGURE 62**

MGTLGQASLFAPPGNYFWS DH SALCF AESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP  
RALEVDSRSVVLLSVVWVLLAPPAAGMPQFSTFHSEN RDWTFNHLTVHQGTGAVYVGAINRV  
YKLTGNLTIQVAHKTGPEEDNKSRYPP LIVQPCSEVLTLTNNVNKLLIIDYSENRLLAGSL  
YQGVCKLLRLDDLFI LVEPSHKKEHYLSSVNKTGTMYGVI VRSEGEDGKLFIGTAVD GKQDY  
FPTLSSRKLPRDP ESSAMLDYELHSD FVSSLIKIPSDTLALVSHFDIFYIYG FASGGFVYFL  
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP  
GDSL AQAFNITSQDDVLFAIFSKGQKQYHHPPD DSALCAFP IRAINLQIKERLQSCYQGEGN  
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG  
YSVVVFGTKSGK LKKVRVYEFRC SNAIHLLSKESLLEGSYWWRFN YRQLYFLGEQR

### **Signal sequence:**

amino acids 1-32

### **Transmembrane domain:**

amino acids 71-87

### **N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

### **Casein kinase II phosphorylation site.**

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534

### **N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509



## **FIGURE 64**

MTTWSLRRRPARTLGLLLLVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFW  
IFGGSIHVFRVPREYWRDRLLKMKACGLNTLTITYVPWNLHEPERGKFDFSGNLDLEAFVMA  
ABIGLWVILRPGPYICSEMDLGGLP SWLLQDPGMRLRTTYKGFT EAVDLYFDHLSRVVPLQ  
YKRGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLLTSDNKDGLSKGIVQGVLAT  
INLQSTHELQLLTIFLFNVQGTQPKMVM EYWTGWFD SWGGPHNILDSS EVLKTVSAIVDAGS  
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTA KYMKLRDFFGSISGIP  
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENL FVNGNGQSFGYILYE  
TSITSSGILSGHVHDRGQVFVNTV SIGFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGEN  
IDDQRKGLIGNLYLNDSP LKNFRIYSLDMKKSFFQRFGLDKWXS L PETPTLP AFFLGSL SIS  
STPCDTFLKLEGWEKG VVFIN GQNLGRYWNIGPQKTL YLPGPWLSSGINQVIVFEETMAGPA  
LQFTETPHLGRNQYIK

### **Signal sequence:**

amino acids 1-27

### **Casein kinase II phosphorylation site.**

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

### **N-myristoylation site.**

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,  
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586



0000000000

GGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC  
CTGTGTAGGGTCTCTACTTTGGCCCTTCGTGGGGGTCAAGACGCGAGCCACTAGCCCAAAGG  
GGAGCAAGACCGGGCTCGGCCCGAGGCCCGGACGACCTTCATCTCCCAATTGTTGGAGAATC  
CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC  
AAGAAGCTGTCTTCGCTTCGTTCCTCGTGTGCGCGCTCAGCGCTACGACTCTGCTGCCCA  
GGCAGACACTCGTCTGTTCGTAGTGATAGGGGTATGACCGGTTTCTCTAGACGGGGCC  
CGTTCGCTATGTGTCTGGCAGCCTGCACATACTTCGGGTACCGCGGGTGCTTTGGGCCGA  
CGGCTTTTGAAGATGCGATGGAGCGGCCCTCAACGCCATACAGTTTATGTGCCCTGGAATC  
CCACGAGCAGACGCTGGGGTCTATACTTTAATGGCAGCCGGGACCTCATGCTCTTCGTA  
ATGAGCGAGCTCTAGGCAACTCTTGTTGCTACTAGACAGCAGGACCTTACATCTGTGCAGAG  
TGGGAGATGGGGGTCTCCCATCTCGTGTCTCGAAAGCTGAAATCTACTAAGAACCCTC  
AGATCCAGACTCTCTTCCCGCAGTGGACTCTGGTTCAAAGGCTTGTCTGCCCAAGATATATC  
CATGCTTTATCAAAATGGGGCAACATCATAGCAATCAGGTGGAGAATGAAATATGGTAGC  
TACAGACCTGTGACTTCAGCTACATGAGCAGCTTGGCTGGGCTTCTCGGTGCACTGTAGG  
AGAAAAGATCTTGCTCTTCACCACAGATGGGCCCTGAAGGACTCAAGTGTGGCTCCCTCGGG  
GACTCTATACCACTAGATATTTGGCCCGGCTGACAACATGACCAAAATCTTACCTTGCTCT  
CGGAAGTATGAACCCCATGGGCCATTTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA  
CTGGGGCCGAAGATCACTCCACCGGTCTGTGTGCACTGTAAACAAAGGACTAGAGAACATGC  
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGG  
AATGTCGCCGATAAGAAGGGGACGCTTCCTTCGATTACTACCAGCTATGACTATGATGCAC  
TATATCTGAAGACGGGGACCCACCACTAAGCTTTTGTCTCTCGAGATGTCAATCAGCAAGT  
TCAGGAAGTCTCTTTGGGACCTTTACTCTCCCGAGGCCCAAGATGATGCTGGACCTGTG  
ACTCTGCACCTGGTTGGGCATTTACTGGCTTCTCTAGACTTGCTTTGGCCCCGTGGGCGTAT  
CTATTCATCTTGGCCAAATGACCTTTAGGCTGTCAAGCAGGACCACTGGCTTCATGTTGTACC  
GAACCTATATAGCCCATACATTTTGGAGCCAACCACTTCTGGGTGGCCAAATATGGAGTC  
CATGACCTGCTGCTATGTGATGGTGTGATGGGGTGTTCAGGGTGTGTGGAGCGCAATATGAG  
AGACAAACTATTTTGTACGGGAACTGGGGTCCAACTGGATATCTTGGTGGAGCAACTGG  
GGAGCTCAGCTTTTGGGTCTAACACGAGTGACTTCAAGGGCTGTGTTGAAGCCAACTTCTG  
GGGCAAAACATCTTACCACGTGGATGATGTCTCCCTCTGCAAAATTGATAACCCTGTGAAGT  
GTGGTTTCCCTCCAGTTGCCAAATGGCCATATCTCAAGCTGTCTTGGGCCCAACTCT  
ACTCCAAACATTTCCAATTTTAGGCTCAGTTGGGACACATTTCTATATCTACCTGGATGG  
ACCAAGGGCCAACTCTGGATCAATGGGTTTAACTTGGGCGGCTATGGACAAAGCGGGCC  
ACAAACAGCCCTCTACGTGCCAAGATTCCTGCTGTTTCTAGGGGAGCCCTCAAACAAATTA  
CATTGCTGAACTAGAAGATGTACCTCTCAGCGCCCAAGTCAAAATTTGGATAAGCCTATCT  
CTCAATAGCACTAGTACTTTGCAAGGCACATATCAATTCCTTTCACTGTACATACACTGAG  
TGCCTCTGAACCAATGAGATTTAAGTGGGCAC**TGA**AAGGTAGGCCGGGCACTGGTGGCTCATGC  
CTGTAATCCGCAACACTTTGGGAGGCTGAGACGGGGTGATCTCAAGGTCAAGGACTCTCAAGA  
CCAGCTTGGCCCAACTGTTGAAACCCCTCTCCAATAAAATTAACAAATTAGCCGGGGTG  
ATGGTGGGCACCTCTAATCCAGCTACTTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC  
AGAGGACGAGGTTTGCAGTGAAGTGGAGGTTGTACCACTGCATCTCCAGCTTGCTGACAGTGA  
GACACTCCACTCTCAAAAATAAAAAA

## **FIGURE 66**

MAPKKLSCLRSLLPLSLTLLLPQADTRSFVVDGRGHRFLLDGAPFRYVSGSLHYFRVPRVL  
WADRLMKRWSGLNAIQFYVPWNYHEFPQGVYNFNNGSRDLIAFLNEAALANLLVILRPGPYI  
CAEWEMGGILPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE  
YGSYRACDFSVMRHLAFLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDVDFGADNMTKIF  
TLRLKYEHPGHLNVNSEYITGWLDYWGQNHSTRSVSAVTKGLNMLKLGASVNMVMFHGGTNF  
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPSPKMMML  
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVFN  
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP  
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL  
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD  
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

### **Signal sequence:**

amino acids 1-27

### **N-glycosylation site.**

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 4-8

### **Casein kinase II phosphorylation site.**

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,  
603-607, 644-648

### **Tyrosine kinase phosphorylation site.**

amino acids 191-198

### **N-myristoylation site.**

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,  
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

## FIGURE 67

GCTTTGAACACGTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC  
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT  
TTATGGCTTTATCTGCCTCTACACTCTCTTCTGGTTATTGAGGATACCTTTGAAGGAATATT  
CTTTGCAAAAAGTCAGAGAAGAGAGCAGTTTGTAGTACATTCCAGATGTCAAAACGATTTT  
GCGTTCTTCTTACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTTTGGTGTGTT  
CTTGTGAGAAGTTAGTGAATAAACTTAGGGAATTAGTTTGAAACCATGAGTGGACATTTG  
AAAACTCAGGCAGCACATTTACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG  
CTGTCGGGGGTGCCGATGTGTCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC  
AATTCAGAAGCTAAAATTCTGTCTAAGATTTCTCAAATGACTAACCTCCAAGAGCTCCACC  
TCTGCCACTGCCCTGCAAAAGTTGAACGAGACTGCTTTTAGCTTTCTTCGCGATCACTTGAGA  
TGCCTTACAGTGAAGTTCACTGATGTGGCTGAAATTCCTGCCTGGGTGTATTTGCTCAAAAA  
CCTTCGAGAGTTGTACTTAATAGGCAATTTGAACTCTGAAAAAATAAGATGATAGGACTTG  
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCCACGTGAAGAGCAATTTGACCAAAGTT  
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTACATAATGACGGCAC  
TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGTGAGCTGGAACCTCCAGA  
ACTGTGAGCTAGAGAGAATCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAACCTGGAT  
TTAAAGTCCAATAACATTCGCACAATTGAGGAAATCATCAGTTTCAGCATTAAAAACGACT  
GACTTGTTTAAAAATTATGGCATAACAAAATTGTTACTATTCTCCTCTATTACCCATGTCA  
AAAACCTGGAGTCACTTTATTTCTCTAACAACAAGCTCGAATCCTTACCAGTGGCAGTATTT  
AGTTTACAGAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTCCAATAGA  
AATAGGATTGCTTCAGAACCTGCAGCATTGTCATATCACTGGGAACAAAGTGGACATTCTGC  
CAAAACAATTGTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAATGCATCACC  
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGGAACTG  
CTTGAGACCGCTGCCAGCCAGCTGGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTTGTG  
TGGAAGATCACCTTTTGTATACCCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA  
AATATTCCTTTTGCAAATGGGATTAACTAAGATAATATATGCACAGTGATGTGCAGGAAC  
AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG  
ATACATCTTTTAAAAATAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT  
GTTCAATGTTGTAGGGTTTTAAGTCATTCATTTCCAAATCATTTTTTTTTCTTTTGGG  
AAAGGGAAGGAAAAATTATAATCACTAATCTTGGTTCITTTTAAATGTTTGTAACTTGGAT  
GCTGCCGCTACTGAATGTTTACAAATTGCTTGCTGCTAAAGTAAATGATTAAATTGACATT  
TTCTTACTAAAAAAAAAAAAAAAA

## **FIGURE 68**

MAYMLKKLLISYISIIICVYGFCLYTLFWLFRIPPLKEYSFEKVVREESSFSDIPDVKNDFAFLLHMVDQYDQLYSKRFGVFLSEVSENKLRISLNHEWTPEKLRQHISRNAQDKQELHLFMLSGLVPDAVFDLTDLDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLSENKMMIGLESRLRLHLKILHVKSNTLTKVPSNITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAELELQNCLELERIPHAIFSLSNLQELDLKSNNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLESPLVAVFSLQLKRLCDVSYNNISIMPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSGLTQLELKGNCCLDRPLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIPFANGI

### **Signal sequence:**

amino acids 1-20

### **N-glycosylation site.**

amino acids 241-245, 248-252, 383-387

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 326-330

### **Casein kinase II phosphorylation site.**

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

### **Tyrosine kinase phosphorylation site.**

amino acids 349-355, 375-381

### **N-myristoylation site.**

amino acids 78-84, 124-130, 212-218, 392-398

10  
 9  
 8  
 7  
 6  
 5  
 4  
 3  
 2  
 1

CCACAGCGTCGCGGGCTCTCTCTGGACATTGGACATTCCATTCTTTTTCATTGACAAATGCATCTTTTATTTCCT  
TTTTCATCTCTGGGCGAGCTGGGATCTGAGCGCCCTGGCGAAGACATTTTCTTTTACACAATAGAGAT  
TTTCTTTCTGGGTTTCTCTCTCCCTCGACATTGGCATGCTTGTGGTTGTGTGGGGGAGGAGACATCGTGG  
GCTGATGCTGCTCTTGCACTATCTGCGCTAGGATCATCGAATCTTTGGACCTCCATACAGTATGATTCGCTGTC  
ATGCTGCTGTGGTATCTCTGGCGGCTTGCTCTGCTGATAGTGTGCTGCTGTCTTCTTCAAAATACACAAAC  
GCGCTAAAGCGTCCAAAGGAACTCGAAGCTGTGGCTGTGTAAAAATCACACACCGACCAAGTGTGGTGGCCAGG  
AACAGCGCAGGCCAAAACCTGCGACCGAGTCTTGCTGCTGCCCTCGAGTGTGTGAAGGATATAGAAATGTGTGCC  
AGTTTGTGATCTCTGCGCACTTGCTGCTGTGGCAATAAATBAGGGCCCTTGAGTATGGAAGAAGCTCCCTTCTCAA  
CGAGAGCGCTCGAAGATCTCAATGATGTCAATGAGGCCACTGTTTGTGATGTGACGCCACAGAAAGAAAGCCAG  
CTCCCATCAGTTTCTATGAAAGAAATACATCGATGCTGCTGGGAACAGCATGCTGCAATCATCAATCCC  
AGTGAAGAACCTGCACCTGGCACAATAGAAAGACAGAAAGAAACAAAGACATCAGAATATCTTTCTCTATGTCCAGT  
GTCCAGATGTGAAGCTGTGAAAGTGAAATCAATAAAGTCTTTGACGGAACTCCAGCAATGGGCTCTCTGCTAGGG  
CAGTCTGACAGTAAAAACGACTATGTCTCTGTTATTTGAATCATATCCACGTACATAGCATGCTTTCAAATAGTTTACT  
GATTCGACAGAAATTCAAAGAACTGCTTTGTCTGTACTACTCTTTCTCTCTCAAATCTCTATTCTCAAAGTGT  
GGCGGTTTACCTTGATATCTTGAAGGATCTCTCACCAGCCCAATACCCAAAGCCGCATCTTGAGCTGGCTTATT  
TGTGTTGGGCACATCAAGTGGGAGAAAGATTAACAAGATAAAATAAACTTCAAAGAGATTTCTCTAGAAATAGAC  
AAACAGTGTCAAATTTGATTTCTTGCCACTATATGATGGCCCTCCACAACTTGTGGCTGATGTGACAGACTGTGT  
GGCCCTGTGATCTCCCACTTCGAACTGCTCATCAAATCTCTGATCGTGTGTGCTACAGATATAGCAATCT  
TACCGGGGATTTCTGCTCTCTCACTCAAATTTATGACAGAAACATCAACATACATCTTTAACTTGCTCTCT  
GCAGGATGAGAGATTATTAAGCAAACTCTACTTACGAGGCTTTTAACTCTAATGGGAAATCACTGCAATAAAA  
GACCCCACTTGCAGACCAAAATTTACAAATTTGTGGAAATTTCTGCTCCCTCTAAATGGATGTGGTACAATCAGA  
AAGTGAAGAATCAGTACAATCTTACACAAATAATACCTTTTCTGCACTCAAATCTGAAAGTATCCAACT  
CGCTGACAAACCACTCCGATATTGTGAGATGTGAAATGGGACATAATCTACAGCTGGAGATTAATACATTAACA  
GAGATAGTATGTAATACAAGTCAAAATGAGCTGGGCAATAATACACAGTACAGTCTTTTGTAACTCAAATCA  
TTTGAAGAAGACTATATCTGAAATCACCATATTTGTGGATTTGAAACCAAATCTTTTGTTCAAATGTAGTCTGCAC  
ACCTCAGATCAAATTTGTGGTGTGTTCTTGATACCTGAGAGCTCTCCCACTCTGATCTTGATCTTCAACCT  
TAGACCTTAATCAAGAGTGGATGTAGTGCAGATAGAACTGTGAAGTGTATCCCTTATTTGGACACATGGGGAGA  
TTCAGTATTAAATGCTTTAAATTTCTGAGAAGTATGAGCTCTGTGATCTCGAGTGTAAAGTTTGTATGTGTGAT  
AGCAGTGACACCAAGTCTGCTGCTCAATCAGGTTTGTGCTCCAGAGCAAAACAGACGATCTTTCTATATAATGG  
AAACAGCATCTTCATCATTAGAGGCCATTCTGTAAGAGGATCGAAGTGGCAATTCAGGATTTCAGCAT  
GAAACACATCGGGAAGAACTCCAAACAGGCTTTTCAACAGTGTGACATGTTTTCCTTACGGTCTAGCTGCTG  
AATGTGGTGAAGTAGGCAATACAGTGAAGCATTTTGTAAATCAAGGGCAGATACAATAACACGAGAGCTG  
CAGAACTATTAACTAACAGGCTCCAACCTTAAGTGTAGACATGTTTCTCCAGATCGCAAAGGAAATGCTACTCGT  
GGCTACAATATATGAAATAAGTAGGAAGGGCTCGAAGTGTGACACAGGCTGTGATGTGAAATAAAAA

## **FIGURE 70**

MELVRRIMPLTLILLSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI  
ERPENKSIRIIIFSIVQLDPDGSCSENIKVFDDGTSSNGPLLGGVCSKNDYVPVFESSSSSTLT  
FQIVTDSARIQRTVFVFYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHELAYCVVWHIQV  
EKDYKIKLNFKEIFLEIDKQCKFDFLAIYDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVLS  
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVVISKSYLEAFNSNGNNLQLKDPTCRP  
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIIVKCEMGHNST  
VEIIYITEDDVIQSNALGKYNTSMALFESNSFEKTILESPYYVDLNTLQVQVSLHTSDPN  
LVVFLDTCRASPTSDFFASPTYDLIKSGCSRDETCVYPLFGHYGRFQFNAFKFLRSMSSVYL  
QCKVLICDSSDHQSRNCNGCVSRSKRDISSYKWKTDSSIIGPIRLKRDRSASGNSGFGHETHA  
EETPNQPFNSVHLFSFMVLALNVVTVATTVRHFVNQRADYKYQLQNY

### **Signal sequence:**

amino acids 1-24

### **Transmembrane domain:**

amino acids 571-586

### **N-glycosylation site.**

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423

### **Casein kinase II phosphorylation site.**

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560

### **Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

### **N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG  
GGACATGCGGGCCCCAGGAGCTCCCGAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGCTGC  
TGCTGCGCCGCGCCGCGTGCCTGCCCCACAGCGCCACGCGCTTCGACCCCACTGGGAGTCC  
CTGGACGCCCGCCAGCTGCCCGCGTGGTTTGACCAGGCCAAGTTCGGCATCTTTCATCCACTG  
GGGAGTGTTTTCCGTGCCCAGCTTCGGTAGCGAGTGGTTCTGGTGGTATTTGGCAAAAGGAAA  
AGATACCGAAGTATGTGGAATTTATGAAAGATAATTACCCTCCTAGTTTCAAATATGAAGAT  
TTTGGACCACTATTTCACAGCAAAATTTTTTAAATGCCAACCCAGTGGGCAGATATTTTTCAGGC  
CTCTGGTGCCAAATACATTGTCTTAACTTCCAAACATCATGAAGGCTTTACCTTGTGGGGGT  
CAGAATATTCTGTGGAACCTGGAATGCCATAGATGAGGGGCCCAAGAGGGACATTGTCAAGGAA  
CTTGAGGTAGCCATTAGGAACAGAAGTGCACCTGCGTTTTGGACTGTACTATTCCTTTTTTGA  
ATGGTTTTCATCCGCTCTTCTTGGAGGATGAATCCAGTTCATTCCATAAGCGGCATTTCCAG  
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATATCAGCCTGAGGTTCTGTGG  
TCGGATGGTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCTGGTT  
ATATAATGAAAGCCAGTTTCGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA  
TCTGTAAGCATGGTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA  
CATAAATGGGAAAACCTGCATGACAATAGACAAAACCTGTCTGGGGCTATAGGAGGGAAGCTGG  
AATCTCTGACTATCTTACAATTGAAGAAATGGTGAAGCAACTGTAGAGACAGTTTCATGTG  
GAGGAAATCTTTTGATGAATATTGGGCCCACACTAGATGGCACCATTCTGTAGTTTTTGGAG  
GAGCGACTGAGGCCAAGTGGGGTCTGGCTAAAAAGTCAATGGAGAAGCTATTTATGAAACCTA  
TACCTGGCGATCCCAGAATGACACTGTACCCCCAGATGTGTGGTACACATCCAAGCCTAAAG  
AAAAATTAGTCTATGCCATTTTTCTTAAATGGGCCACATCAGGACAGCTGTTCCTTGGCCAT  
CCCCAAGCTATTCTGGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAACTG  
GATTTCTTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACATTATCAGATGC  
CGTGTAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG  
ATGCTGCAAGTTATGTCTAAGGCTAGGAACTATCAGGTGTCTATAATTGTAGCACATGGAGA  
AAGCAATGTAACTGGATAAGAAAATTAATTTGGCAGTTTCAGCCCTTTCCCTTTTTCCCACTA  
AATTTTTCTTAAATTACCCATGTAAACCATTTAACTCTCCAGTGCACTTTGGCCATTAAAGTC  
TCTTCACTGATTGTGTTTCCATGTGTGACTCAGAGGTGAGAAATTTTTTCACTTATAGTAG  
CAAGGAATGGTGGTATTATGGACCGAACTGAAAATTTTATGTTGAAGCCATATCCCCATG  
ATTATATAGTTATGCATCACTTAATATGGGGATATTTTCTGGGAAATGCATTGCTAGTCAAT  
TTTTTTTTGTGCCAACATCATAGAGTGTATTTACAAAATCCTAGATGGCATAGCCTACTACA  
CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG  
AATACTGTAGGCAATAGTAACAGTGGTATTTGTATATCGAAACATATGGAAACATAGAGAAG  
GTACAGTAAAAAAGTCTGAAAAATAATGGTGCACCTGTATAGGGCACTTACCACGAATGGAG  
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAAGGCTGTGAAGCCTAGGACATTA  
TTGAACACTGCCAGACGTTATAAAATCTGTATGCTTAGGCTACACTACATTATAAAAAAA  
GTTTTTCTTTCTCAATTATAAATAAATCAAGTGTACTGTAACTTTACAAACGTTTTAATT  
TTAAAAACCTTTTTGGGCTCTTTTGTATAACAATTGCTTAAACATAAACTCATTGTGCAA  
ATGTAA

000000.071501

## **FIGURE 72**

MRPQELPRLAFPLLLLLLLLLPPPPCPAHSATRFDPPTWESLDARQLPAWFDQAKFGIFIHWG  
VFSVPSFGSEWFWWWYQKEKIPKYVEFMKDNYPSPSKYEDFGPLFTAKFFNANQWADIFQAS  
GAKYIVLTLSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLEW  
PHPLPLEDESSSPHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY  
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI  
SDYLTIEELVKQLVETVSCGNNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT  
WRSQNDTVPDVPVYTSKPKEKLVAIFLKWPTSGQLFLGHGPKAILGATEVKLLGHGQPLNWI  
SLEQNGIMVELPQLTIHQMPCKGWALALTNVI

### **Signal sequence:**

amino acids 1-28

### **N-glycosylation site.**

amino acids 171-175, 239-243, 377-381

### **Casein kinase II phosphorylation site.**

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,  
375-375

### **Tyrosine kinase phosphorylation site.**

amino acids 361-369, 389-397

### **N-myristoylation site.**

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

### **Leucine zipper pattern.**

amino acids 410-432

### **Alpha-L-fucosidase putative active site.**

amino acids 283-295



## FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGAGCAGTGAGTGTGAGCCTCAACATAGT  
TCCAGAACCTCTCCATCCGGACTAGTTATTTGAGCATCTGCCCTCTCATATCACCAGTGGCCATC  
TGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCTCGGTGTTG  
CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCT  
TTCCATCCAGGTGTCTATGCAGAATTATGGGGATCACCTTGTGAGCAAAAAGGCGAACCCAGC  
AGCTGAATTTACAGAAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG  
GACCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAAACTTGCGAGCTATGGCTGGGTGGGAGA  
TGGATTCTGGTGTATCTCTAGGATTAGCCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTG  
TCTGTATTTGGAAAGGTTCCAGTGAGCCGACAGTTTGAGCCTATTGTTTACAACCTCATCTGAT  
ACTTGGACTAACTCGTGCAATTCAGAAATTATCACCACCAAGATCCCATATTCAACACTCA  
AACTGCAACACAAACACAGAATTTATTGTGAGTACAGTACCTACTCGGTGGCATCCCCCTT  
ACTCTACAATACCTGCCCTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGG  
AGAAAAAATTGATTTGTGTACAGAAGTTTTTATGAAAACTAGCACCATGTCTACAGAAAC  
TGAACCAATTTGTTGAAAAATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTCTC  
CCACGGCTCTGCTAGTGCTTGTCTCTCTCTTTTGGTGTGTCAGCTGGTCTTGGATTTTGC  
TATGTCAAAAGGTATGTGAAGGCCCTCCCTTTTACAAAACAAGATCAGCAGAAGGAAATGAT  
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGA  
AAACTGATAAAAAACCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCGATGCTGGAA  
GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCC  
TTACCTCGCCCCAGCTGGGGAAATCAAAGGGCCAAAGAACCAAGAAAGAAAGTCCACCCCTT  
GGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGC  
CCTTCTCCTTATTGTAAACCTGTCTGGATCCTATCCTCTACCTCCAAAGCTTCCCAAGGCC  
TTTCTAGCCTGGCTATGTCTTAATAATATCCACTGGGAGAAAGGAGTTTTGCAAGATGCAA  
GGACCTAAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCCTCTGGCTGTCTGAGGCTAGG  
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCCGAGCTCAGAC  
CCTTCTCCTTACGCTCTGAAAGAGAAACACGTATCCCACTGACATGTCCCTCTGAGCCCGGTA  
AGAGCAAAAGAATGGCAGAAAAAGTTTAGCCCCGAAAGCCATGGAGATTCTCATAACTTGAG  
ACCTAATCTCTGTAAAGCTAAAAATAAGAAATAGAACAAGGCTGAGGATACGACAGTACACT  
GTCAGCAGGAGCTGTAAACACAGACAGGGTCAAAGTGTCTTCTGAAACATTGAGTGTGA  
ATCACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT  
AGGAAATATACTTTTACAAGTAACAAAAATAAAACTCTTATAAATTTCTATTTTATCTGA  
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCA  
ACAAACATTTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTCTGTAAT  
TGAATATTATTTCTCAAAAAATTGCATAGTAGAAGCTATCTGGGAAGCTATTTTCTCA  
GTTTGTGATTTCTAGCTTACTACTTCCAACTAATTTTATTTTGTGCTGAGACTAATCTT  
ATTCAATTTCTCTAATATGGCAACCATTATAACCTTAATTTATTATTAACATACCTAAGAAG  
TACATTTGTACCTCTATATACCAAGCACATTTTAAAAGTGCCATTAAACAAATGTATCACTA  
GCCCTCCTTTTCCAAAGAAGGAGCTGAGAGATGCGAAATATTGTGCAAAAAATTA  
AGCATTAGAAAACTT

## **FIGURE 74**

MARCFSLVLLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR  
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLIWKVPVSRQF  
AAYCYNSSDTWTNSCIPEIIITKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTPP  
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAPKNEAAGFGGVPTALLVLALLFF  
GAAAGLGFCYVKRYVKAFPFNTNKNQQKEMIE TKVVKEEKANDSNPNEESKTKDNPEESKSP  
SKTTVRCLEAEV

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 235-254

### **N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

### **Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

### **Tyrosine kinase phosphorylation site.**

amino acids 79-88

### **N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## FIGURE 75

AGATGCGGGTCTTGGCACCTCTAATTGCTCTCGTGATTTCGGTGCCGCGACTTTCACGATGG  
CTCGCCCAACCTTACTACCTTCTGTCGGCCCTGCTCTCTGCTGCCTTCTTACTCGTGAGGAA  
ACTGCCGCGCTCTGCCAGGTCTGCCACCCAACGCGAAGACGGTAACCCGTGTGACTTTG  
ACTGGAGAGAAGTGGAGATCCTGATGTTTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA  
TCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAACACAAT  
TCTTTTCTCCGCTTGGATATTGCGATGGGCCTACTTTACATCACACTCTGCATAGTGTTC  
TGATGACGTGCAAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA  
ACCATTGATGAGGAAGTAGAACGGGACAAGAGGGTCACCTGGATTGTGGAGTTCCTTTGCCAA  
TTGGTCTAATGACTGCCAATCATTTGCCCTATCTATGCTGACCTCTCCCTTAAATACAAC  
GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC  
AAAGTGAGCACATCACCCCTCACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGTGGCAA  
GGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTG  
AGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAAACTATCA  
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCAACACAGTGTGAGA  
TGGGGAAAACAAGAAGGATAAATAAGATCCTCACTTTGGCAGTGCTTCCTCTCTGTCAATT  
CCAGGCTCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTTNATTNATGTTTTCCCTTTGG  
CTGNGACTGNGTGGGGCAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAG  
GCACCCCTACAGGAAGGCCTGCCATGCTGTGGCCAAGTGTTCCTGAGGCAAGAAAGAGATC  
TCATAGGACGGAGGGGAAATGGTTTCCCTCCAAGCTTGGGTGAGTGTGTTAACTGCTTATC  
AGCTATTGAGACATCTCCATGGTTTCTCCATGAACTCTGTGGTTTCATCATTCTCTTAG  
TTGACCTGCACAGCTTGGTTAGACCTAGATTTAACCCTAAGGTAAGATGCTGGGGTATAGAA  
CGCTAAGAATTTCCCCAAGGACTCTTGCTTCCTTAAGCCCTTCTGGCTTCGTTTATGGTC  
TTCATTAAAGTATAAGCCTAACTTTGTGCTAGTCTTAAGGAGAAACCTTTAACCACAAAG  
TTTTTATCATTGAAGACAATATTGAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAA  
TAGAGGCTTGAGACTTTCCTTTGTGTGGTAGGACTTGGAGGAGAAATCCCCTGGACTTTCAC  
TAACCTCTGACATACTCCCCACACCCAGTTGATGGCTTTCGGTAATAAAAGATTGGGATT  
TCCTTTTG

## **FIGURE 76**

MAVLAPLIAIVYSVPRLSRWLAQPYLLSALLSAAFLIVRKLPPLCHGLPTQREDGNPCDFD  
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL  
MTCKPPLYMGPEYIKYFNDKTI DEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYN C  
TGLNFGKVDVGRYTDVSTRYKVSTSP LTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE  
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

### **Signal sequence:**

amino acids 1-48

### **Transmembrane domain:**

amino acids 111-125

### **N-glycosylation site.**

amino acids 165-169, 185-189

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 154-158, 265-269

### **Casein kinase II phosphorylation site.**

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

### **N-myristoylation site.**

amino acids 188-194, 225-231

### **Myb DNA-binding domain repeat signature 1.**

amino acids 244-253

## FIGURE 77

GGACAGCTCGCGGCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCTGGGGACGTTTGCCCTG  
GGGCCCCAGCCTGGCCCCGGTCAACCTGGCATGAGGAGATGGGCCCTGTTGCTCCTGGTCCCA  
TTGCTCCTGCTGCCCGGCTCCTACGACTGCCCTTCTACAACGGCTTCTACTACTCCAACAG  
CGCCAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG  
TGGTGGAGACACCCGAGGAGACCTGTTTACCTACCAAGGGGCCAGTGTGATCCTGCCCTGTC  
CGCTACCGTACGAGCCGGCCCTGGTCTCCCCGCGCGTGTGCGTGTCAAATGGTGGAGCT  
GTCGGAGAACGGGCCCCAGAGAAGGACGTGCTGGTGGCCATCGGGCTGAGGCACCGCTCCT  
TTGGGGACTACCAAGGCCGCGTGCACCTGCGGCAGGACAAAGAGCATGACGTCTCGCTGGAG  
ATCCAGGATCTGCGGCTGGAGGACTATGGGCGTTACCGCTGTGAGGTCAATTGACGGGCTGGA  
GGATGAAAGCGTCTGGTGGAGCTGGAGCTGCGGGGTGTGGTCTTTCCCTTACCAGTCCCCCA  
ACGGGCGCTACCACTTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCGGTG  
GTGGCTCCTTTGAGCAGCTCTTCCGGGCTGGGAGGAGGGCCTGGACTGGTGCACGCGGG  
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGGCAGCCCTGCGGTGGCC  
CAGGCTTGGCACCCTGGCGTGCAGGCTACGGCCCCCGCCACCGCCGCTGCACCGCTATGAT  
GTATTCTGCTTCGCTACTGCCCTCAAGGGGCGGGTGTACTACCTGGAGCACCTTGAGAAGCT  
GACGCTGACAGAGGCAAGGGAGGCCCTGCCAGGAAGATGATGCCAGATCGCCAAGGTGGGAC  
AGCTCTTTCGCGCTGGAAGTTCATGGCCTGGACCGCTGCACGCTGGCTGGCTGGCAGAT  
GGCAGCGTCCGCTACCTGTGGTTCACCCGCATCCTAACTGTGGGCCCCCAGAGCCTGGGGT  
CCGAAGCTTTGGCTTCCCCGACCCGAGAGCCGCTTGTACGGTGTATTACTGCTACCGCCAGC  
ACTAGGACCTGGGGCCCTCCCTGCCGCATTCCCTCACTGGCTGTGTATTTATTAGTGGTT  
CGTTTTCCCTGTGGGTTGGAGCCATTTTAACTGTTTTATACTTCTCAATTTAAATTTTCT  
TTAAACATTTTTTACTATTTTTTGTAAAGCAAACAGAACCCAAATGCCTCCCTTGCTCCTG  
GATGCCCACTCCAGGAATCATGCTTGTCTCCCTGGGCCATTGTGCGTTTGTGGGCTTCTG  
GAGGGTTCCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGTGCCAGAGTGGGC  
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGGCATGGTGGGCACAGTTCTCCCTGCCCT  
CAGCCTGGGGGAAGAAGAGGGCCTCGGGGCCCTCCGGAGCTGGGCTTTGGGCTCTCCTGCC  
CACCTCTACTTCTCTGTGAAGCCGCTGACCCAGTCTGCCACTGAGGGGCTAGGGCTGGAA  
GCCAGTTCTAGGCTTCCAGGCGAAATCTGAGGGAAGGAAGAACTCCCTCCCGGTTCCCT  
TCCCTCTCGGTTCCAAAGAAATCTGTTTTGTTGTCAATTTGTTTCTCCTGTTTCCCTGTGTGG  
GGAGGGCCCTCAGGTGTGTACTTTGGACAATAAATGGGTGCTATGACTGCCTTCCGCCAA  
AA  
AA

## **FIGURE 78**

MGLLLLVLPLLLPGSYGLPFYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ  
GASVILPCRIRYEPALVSPRRVRVKWWKLSENGAPEKDV LVAIGLRHRSFGDYQGRVHLRQD  
KEHDVSLEIQDLRLLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ  
VCAEQAAVVASFQQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR  
HRLRHRYDVFCFATALKGRVYYLEHPEKLTLEAREACQEDDATIAKVGQLFAAWKFHGLDR  
CDAGWLADGSVRYPVVHHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

### **Signal sequence:**

amino acids 1-17

### **Casein kinase II phosphorylation site.**

amino acids 29-33, 53-57, 111-115, 278-282

### **Tyrosine kinase phosphorylation site.**

amino acids 137-145

### **N-myristoylation site.**

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

**Figure 1**

GGAGAGCGGAGCGCAAGACTGGATAACAGGGGACCGATGATGTGGCGACCATCAGTTCTGCTGCTTCTGTGTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCAGACGCAGGCCCTCATGGCCAGGGGAGGGTGACCAGGCGGCCCCCTGAGCGACGCTCCCATGATGACGCCACGGGAACTTCAGTACGCCATGAGGCTTTCCTGGGACGGGAAGTGGCCAAGGAATTGCACCAACTCACCCAGAGAAAGCCAGGCCCCGTCTGGGCGGATCTGGAACCGCATGGACCGCGCGGGGGACGGCGACGGCTGGTGTGCTGGCCGAGCTTCGCGCGTGGATCGCGCACACGCAGCAGCGGACATACGGACTCGGTGAGCGCGGCTGGGACACGTACGACACGGACCGGACGGCGGTGTGGGTTGGGAGGAGCTGCGCAACGCCACCTATGGCCACTACGCGCCCGGTGAAGAATTTATGACGTGGAGGATGCAGAGACCTACAAAAGATGCTGGCTCGGGACGAGCGGCGTTCCGGGTGGCGACCAAGGATGGGGACTCGATGGCCACTCGAGAGGAGCTGACAGCCTTCCTGCACCCCGAGGAGTTCCTCACATGCGGGACATCGTGATTCTGAAACCTTGAGGACCTGGACAGAAACAAAGATGGCTATGTCCAGGTGGAGGAGTACATCGCGATCTGTACTCAGCCGAGCCTGGGGAGGAGGAGCCGGCTGGGTGCAGACGGAGAGGCAGCAGTTCGGGACTTCGGGATCTGAACAAGGATGGGCACCTGGATGGGAGTGAGGTGGGCCACTGGTGCTGCCCCCTGCCAGGACCAGCCCTGTGTGAAGCCAACACCTGCTGCACGAGAGCGCACGGACAAGGATGGGCGGTGAGCAAAGCGAAATCCTGGGTAATTGGAACATGTTTGTGGGCAGTCAGGCCACCAACTATGGCGAGGACCTGACCCGGCACACGATGAGCTGTGACACCGCGCACCTGCCACAGCCTCAGAGGCCGCGACAATGACCCGAGGAGGGGGCCGCTGTGGTCTGGCCCCCTCCTGTCCAGGCCCCGCGAGGAGCGAGATGCAGTCCCAGGCATCCTCCTGCCCTTGGGCTCTCAGGGACCCCCCTGGGTGCGGCTTCGTCCCTGTCAACCCCCAACCCAGGGAGGGGCTGTATAGTCCAGAGGATAAGCAATACCTATTCTGACTGAGTCTCCAGCCAGACCCAGGGACCCCTTGCCCCAAGCTCAGCTCTAAGAACCGCCCAACCCCTCCAGCTCCAATCTGAGCCTCCACCACATAGACTGAAACTCCCTGGCCCCAGCCCTCTCCTGCTGGCTGGCCCTGGGACACCTCCTCTCTGCCAGGAGGCAATAAAGGCACGCGCGGACCTTGAAAAA

## **FIGURE 80**

MMWRPSVLLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR  
EVAKEFDQLTPESQARLGRIVD RMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT  
YDTRDRGRVGWEEELRNATYGHYAPGEEFHDVEDAETYKMLARDERRFRVADQDGD SMATRE  
ELTAFLHPPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSABPGEEEPANVQTERQQ  
FRDFRDLNKGHLDGSEVGHWVLP PAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV  
GSQATNYGEDLTRHDEL

### **Signal sequence:**

amino acids 1-20

### **N-glycosylation site.**

amino acids 140-144

### **Casein kinase II phosphorylation site.**

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302

### **N-myristoylation site.**

amino acids 263-269, 311-317

### **Endoplasmic reticulum targeting sequence.**

amino acids 325-330



## FIGURE 81

GGGGCCTTGCCCTTCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG  
GCGGCGGGCGCGGGTGCAGAGGATCCCTGACGCCCTCTGTCCCTGTTTCTTTGTTCGCTCCAG  
CCTGTCTGTCTGTTGTCGCCCCCGCCTCCCGCGGTGCGGGGTGCACACCGATCCTG  
GGCTTCGCTCGATTTCGCCCGAGGCGCCTCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG  
CGGGTCGTCTGTGTCCTCTCTCCTTCGCGCCGCCCGGGGATCCGAAGGTCGCGGGCTCT  
GAGGAGGTGACGCGCGGGGCTCCCGCACCTGGCCTTGCCCGCATTCTCCCTCTCTCCAG  
GTGTGAGCAGCCTATCAGTCAC**ATG**TCCGCACTCGGATCCGGCTCTCGGCCTCGGTGTG  
TGTCTGTCTGCTGCGCGGGGCCGCGGGCAGCGAGGGAGCCGCTCCCATTGCTATCACATG  
TTTACAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCAGGGGGCTGCC  
CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGG  
GCTGCTGTCCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC  
TGGTCGAGAAAATATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAAATGCTTTCTAGAT  
GGTCTGCTTCTTTCACAGTAATCAAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA  
GTGTCCACAGCACATCCACCAACAGGTAACGACTAAAGAAAACCCCGAGAAGAAAATGG  
CAATAAGATTGTAAAGCAGACATTGCATTCTGATTGATGGAAGCTTTAATATTGGGCAGC  
GCCGATTAAATTTACAGAAGAATTTTGTGGAAAAGTGGCTCTAATGTTGGGAATTGGAACA  
GAAGGACCATATGTGGGCTTGTTCAGCCAGTGAACATCCCAAAATAGAATTTTACTTGAA  
AAACTTTACATCAGCCAAAGATGTTTTGTTTGGCAATAAGGAAGTAGGTTTCAGAGGGGTA  
ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATCTTCCAGGTAGATGCTGGA  
GTAAGAAAAGGGATCCCAAAAGTGGTGGTGATTTATTGATGGTTGGCCTTCTGATGACAT  
CGAGGAAGCAGGCATTTGTGGCCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGCCA  
AGCCTATCCCTGAAGAACTGGGGATGGTTCAGGATGTACATTGTGTGACAAGGCTGTCTGT  
CGGAATAATGGCTTCTTCTTACCACATGCCAACTGGTTTGGCACCACAAAATACGTAAA  
GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACT  
CAGTGAACATTGCCTTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTTCCGCCTC  
ATGCTTGAATTTGTTTCCAACATAGCCAAGACTTTTGAATCTCGGACATTGGTGCCAAGAT  
AGCTGCTGTACAGTTTACTTTATGATCAGCGCACGGAGTTCAGTTTCACTGACTATAGCACA  
AAGAGAATGTCCTAGTCTCATCAGAAACATCCGCTATATGAGTGGTGAACAGCTACTGGT  
GATGCCATTTCTTCACTGTAGAAAATGTGTTTGGCCCTATAAGGGAGAGCCCCAACAGAA  
CTTCTAGTAATTGTACAGATGGGCAGTCTCTATGATGATGTCCAAGGCCCTGCAGCTGCTG  
CACATGATGCAGGAATCATTATCTTCTGTGTGGTGTGGCTTGGGCACCTCTGGATGACCTG  
AAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTCTTCCACAAGAGAGTTCACAGGATT  
AGAACCAATTTGTTCTGATGTCTCAGAGGCATTTGTAGAGATTTCTAGAATCCAGCA**AT**  
**AA**TGGTAAACATTTTGACAACCTGAAAGAAAAGTACAAGGGGATCCAGTGTGTAATTTGTATT  
CTCATAACTGAAATGCTTTAGCATACTAGAATCAGATACAAAATCTATTAAGTATGTCAC  
AGCCATTTAGGCAATAAAGCACTCCTTTAAAGCCGCTGCCTCTCGTTTACAAATGTCAGTGT  
ACTTTGTTAAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAACTCAGGAAAGAGGA  
GATAATGTGGATTAAAACTTAAGAGTTCTAACCATGCCTACAAATGTACAGATATGCAAA  
TTCATAGCTCAATAAAAGAACTGTACTTTAGACCAAAAAAAAAA

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Signal sequence:

N-glycosylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

Amidation site.

amino acids 145-149



## **FIGURE 84**

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ  
HKLRS AVEEMEAEBAKASSEVNLANLPSPYHNETNTDTKVGNNTIHVHREIHKITNNQTG  
QMVFSETVITSVGDEBGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGRMLCTRDSECCG  
DQLCVWGHCTKMATRGSGNTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGELCHDPASRL  
LDLITWELEPDGALDRPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV  
GSFMEEVRQELEDLERSLTEEMALGEPAAAAAALLGGEET

### **Signal sequence:**

amino acids 1-19

### **N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

### **Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

### **N-myristoylation site.**

amino acids 202-208, 217-223

### **Amidation site.**

amino acids 140-144

AAGAGGCTCTGGGAGAAAGAGGTAAGAAAGTTTAGAGAACCTACCTTCATCTCTTGGGCTCAGAAGGATCTCTG  
AAGATACACATTAATTCAGCCATCTCACTCTCTCCCTCCCAACACACATGTGCATGTATACACACATACATCA  
CACACATACACCTTCTCTCTCTCTACCTGAAGATCAACAGTCACTCTGTGAGCAGGTATATAGAAAGACAC  
TAAGAGCTTTAAGGACAGSGCTGSCCATCTCTGACGCTCTTTGGCTTGTGAGTCAAAAAACATGGGAGGGG  
CCAGGACAGGTTGATCTACACCTGTAAATCCGACCATTTTGGGAGACCGAGGTGAGCAGATCATTTAGGCTCAGGAG  
TTTGAGACAGGCTGGCCGACATGGAGAACTCCCTACTCTACTAAAAATACAAAATTAGCCAGGATGTGTGGC  
AGSTGGCTGTAAATCCAGCTACTCTAGSTGGCTGAGCCAGGAAAGTCGTTGAATCCAGGAGGCGGAGGATGACGT  
CAGCTGATGGTCAGCTGTCATCTCAGCTCGGGTGACAGAAATGAGATCTGTCTCAAAAACACAAACACGGGAGGA  
GGGTGATAGATCTGTTCTCTGCAACCTCTTAATCTGTCATCTCTTCTTCAGGSGTCCGCTCTAGTGGGSGCT  
GCAATAGCTAGACAGGCCAGCCCGGACGAGGACAGAGAGAGGAGATATAGAGGGGGCAAGAGTGAACGCGCG  
GTGTGAATGATGACCTGCGCTGGGAGGGTGGTTCTTGGGCGCTGGCAGGGTGTGACCTTACCTCGTAAAAACACA  
AAGAGCAGGATCTCAGATCTCTCTTGTAATGTGCCCTGGCTCGACCTCACAATGAGGCTTCTCTGTGGCGCCC  
ACTCTCTGACTGTTGGGTGGCTGGTGCACATGCCACTGTCGCTGGTGTACCTGCGATCTGTTCCCTGGCCCCCTCA  
GTGTGCTGTCGAGATCCGGCGCTGGTATAGCTCCGCGCTGTCTTACCCGGAGGCTATACCCTGTGGAATGCAATGA  
CTTATTCTGACGCGAGTCCCCGGGCACTCCCCGAGGACACACAGACCTGCTCTCTCGAGACAGACAGCATTTGT  
CCGTGTGGACAGATGATGAGCTGGGCTACTCTGGCCTAATCTCAGAGCTGGACCTGTCCACAGACAGCTTTTCGGA  
TGCCGAGCTTGTGATTTTCATGTGCTCCCGAGCTCTACAGGCTGCACATAGAGGAGAACCTGACCTGACCCGGT  
GGAGGACACACAGCTTTCTGAGGCTGGCCAGGCTCATAGAAGATCTTATCTCAACCAACACACAGCTTTACCGCATGCG  
CCGAGGGGCTTTTCTGGCCTCAGCAACTTGTCTGGCTGACACTCAATCTCAACCTCTCTGAGGGGCTTGTGACAG  
CAGCTTTTGTAATGTGCTCCCACTGTAGGATGATCTGATGTGGGGCACAACAGGTTAGATGGCATCTCTGGACAT  
CGACTTCCGGCCCTGGCCAACTGCGTAGCTGTGCTGTAGCAGGCATGAACCTGTGCGGAGATCTCCGATCATGCT  
CTGTGAGGGGCTGCAAGGCTGGAGAGCTCTCTCTTTATGACAAACCGCTGGCCGGGTGGCCGCGGGGCTGACAT  
GGACAGTGTGCCGGGCTCAAGTTCTCTAGACCTCAACAAACACCTCCAGCGGTTAGGCGCGGGGATCTTGGC  
CAACATGTCTGACACTTAAGGAGCTGGGATGACATCAACATGTGAGGAGCTGTGCTTCATCAAGCAATTTGCCCTGTG  
GAACCTCCCGAGGTGACAGCTGGCACTACCAATCAACACCGCTGTCTCTATCAACCCCGCCGGCTTCCTG  
CCACTCTGCCAGATGGAGACCTCTCACTCAACAAACGCTCTCAGTCCCTTGACAGCAGACGGCTGAGTCT  
CTGCCCAACCTCAGCAGAGTGAAGTCTCTCCGAGAAACCCCATCCGCTGTGACTGTGTGATCTGGGCGCTACCG  
CACGGGACCCGCTGTGCGCTTCACTGAGCCGCAATCCACCTGTGTGGCGAGCTCTCGGACCTCTCAGGCGCTCCG  
GGTCTGCTGAGTGGCTCTCTCCGGAGAGTACGGGACCACTGTTTGGCCCTCATCTCCCAACCGAAGCTTCCCCCAAC  
CTCTCAGTGTAGCCATGGAGAGGACATGGTGTGTGCTATGCCGGGACCTGGCGAAACCGAAACCCGAGATCTACTG  
GGAGCTCCAGCTGGGCTTGCATGTACATCTGCCATCAGGCGAGGAGTACCGGGTGTACCGGAGGGGACCTT  
GGAGCTCGGAGGGGTGACGACGAGAAGAGGCGGCTATACACTGTGTGCCCAAGAACCTGTGTGGGGCTGACAC  
TGATGCTGGTGAATGTGTGTTGGGCGCTGCTCTCTCTCCAGCAGGACGGGACAGAGAGAGGGCTGTGAGCTTCG  
TAAGCAGAGATACCCACCTTATACATCTGCTATCTTGGGTCACCCCAACACAGACAGTGTCCACAACTCATCT  
CTGGTCTCAGTGGCTCTCTCTCTCCGGGCGAGGGGCGACAGCTCTGGCCCGGCTGCTCTGGGGAAGCCACAGATCT  
CAACATTAACCGCTCTCTCAGGCGACGGAGTATGGGCTGCTGCTCAGTGGGCTTTGTCTGATGCCACACCA  
GTTGGCTGTGATGGGCGAGGACAAAGAGGCCACTTCTGGCCACAGAGCTTAGGGGATGCTCTGGGCTCATCT  
TGCATCTGTGCTCTCGTGTCTCTCTCTCTGGCAGCTGGGCTAGCGGGGCACTTGGCAACGACCCAAACCGAGGA  
GGGTGTGGGTGGGAGGGCGGCTCTCCCTCAGGCTGGGCTCTTGGGGCTGGAGTGGCCCTCTCTGTCCGGTGTGT  
GTCTGCTCGCTCTGCTCGCTCGTAATCAGGAGGAGCTGCCAGATCTCAGAAAGGAGAGACATGTTGGC  
ACCATGTCTCAAAATTTCTGAGAGCTCAGGCTTCTCAGAGATAGAGAAATCACTAGGATCACTTTTACAAA  
AAGAGACAGCTTGGGCGAGTGCCTCTCGAGGAAAGGACATGGACCCAGTGGCTTGTAGGCTCGGACGCTGGGC  
CAAGACAGATAGGGGCTTGTGGCCCTGGGGGTGCTCTGACGCTTGAAGAAATGGCCCTTACCTCTTAGGGTCA  
CTCTCTGCTGCAATCTGAGGAACATCTCCAGGAAAGGAGGAGGATCTTGGTAGAGGCTTACCTGCTCCCATCTTCT  
CTCTCTGGCCAGGAGCTCTCGGCTCTGGCTTGGCTTGGCTCTCTGGGACAGGGCTGAAGGAGGCTCATCATCTCAT  
CTTTCTCTGTAGAGCTCAGTGTGCTTGTCTTGTGCTCTCTGGGACAGGGCTGAAGGAGGCTCATCATCTCAT  
CTGGGCGGGGCTGCCCTCAATGTGGGAGTGACCCAGCCAGATCTGAAGGACATTTGGAGAGAGGGATGTGGCGAGGA  
CGGCTCATCAGCAGGCTGGGCTGGCATTCGAGAGCTGACTTTCTATAGGCAATTTTGTACTCTTGTGGAGAA  
ATGTGTCACTTCCCCAACCCGATTCACTCTTTTCGCTGTTTGTAAAAAATAAAATAAATAATACAAATAAA

## FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA  
VPPALPAGTQTLLQLSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL  
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE  
MLPNLEILMIGGNKVDAILDMNFRPLANLRSVLVLAGMNLREISDYALEBGLQSLESLSFYDNQ  
LARVPRRALEQVPGKFLDLNKNPLQRVGPQDFANMLHLKELGLNNMEELVSIDKFALVNL  
ELTKLDITNNPRLSFIHPRAFHHLPMETLMLNNNALSALHQQTVESLPNLQEVGLHGNPIR  
CDCVIRWANATGTRVRFIEPOSTLCAEPPDLQRLPVREVPFREMTDHCPLISPRSFPPSLQ  
VAGESMVLHCRALAEPEPEIYVWTPAGLRITPAHAGRRYRVYPEGTLELRRTAEAGLYT  
CVAQNLVGADTKTVSVVVGRALLQPGRDEGQGLELRVQETHPYHILLSWVTPPNTVSTNLTW  
SSASSLRGGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS  
CHRALGDRPGLIAILALAVLLLAAGLAAHLGTGQPRKGVGGRRPLPPAWAFWGSAPSVRVV  
SAPLVLPWNPRGKRLPRSSGETLLPPLSQNS

### Signal sequence:

amino acids 1-18

### Transmembrane domain:

amino acids 629-648

### N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

### cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

### Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,  
243-247, 313-317, 488-492, 700-704

### Tyrosine kinase phosphorylation site.

amino acids 532-540

### N-myristoylation site.

amino acids 15-21, 493-499, 566-572

### Amidation site.

amino acids 470-474, 660-664, 692-696



## **FIGURE 88**

MRQTIKVIKFIILICYTVVYVHNKFDVDCTVDIESLTGYRTYRCAHPLATLTKILASFYI  
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSIDPVKNDFAFMLHLIDQYDPLYSK  
RFAVFLSEVSENKLRQLNLNNEWTLDKLRQLTKNAQDKLEHLFMLSGIPDVTVDLVELEV  
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLENLRALHIKFTDIKEIPLWI  
YSLKLTLEELHLTGNLSEAENNRIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI  
NNEGTKLIVLNSLKKMANLLELELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIIEEIIISFQ  
HLHRLTCLKLWYNHAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLPYCRKLRYLDLSHNNLT  
FLPADIGLLQNLQNLAITANRIETLPPPELFQCRKLRLHLGNNVLQSLPSRVGELTNLTQIE  
LRGNRLECLFVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

### **Transmembrane domain:**

amino acids 51-75 (type II)

### **N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

### **Casein kinase II phosphorylation site.**

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497

### **N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447



## FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCCGTACTTGTCAATGGAGCTGGCACTGCGGCGCTCTCCCGT  
CCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCAATTGACT  
GGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCACATG  
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT  
GTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGTGAAACTTTGAGGAAATTGGGC  
CCCTTGACAGTGATCTCAAACCACGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT  
GTGGATAATCCCGTGGGCACTGGGTTCACTTATGTGAATGGTAGTGGTGCCATGCCAAGGA  
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG  
AATTCAGACAGTTCCATTCTACATTTTCTCAGAGTCCATGAGGAGAAAATGGCAGCTGGC  
ATTGGTCTAGAGCTTTATAAGGCCATTGAGGAGGGACCATCAAGTGCAACTTTGCGGGGGT  
TGCCTTGGGTGATTCTGGATCTCCCTGTTGATTCCGTGCTCTCCTGGGGACCTTACCTGT  
ACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA  
CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT  
GATCATTGAACAGAACACAGATGGGGTGAACCTCTATAACATCTTAACTAAAAGCACTCCCA  
CGTCTACAATGGAGTCGAGTCTAGAATTACACAGAGCCACCTAGTTTGTCTTTGTGACGCGC  
CACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA  
GCTCAAAATTATTCTGAGGATCAATCCTGGGAGGCCAGGCTACCAACGTCTTTGTGAACA  
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC  
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTGAGGAGGCCTG  
GGTGCGGAAACTGAAGTGGCCAGAACTGCCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGT  
ACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTC  
TACTGATTCTGAAAGCTGGTCATATGGTTCTTCTGACCAAGGGGACATGGCTCTGAAGAT  
GATGAGACTGGTGACTCAGCAAGAAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCT  
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCT  
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGAGAGGATAAAAATCATTGTCTCT  
GGAGGCAATTTGGAATAATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGAT  
TTGTTTTGATCAAAATAAAGGATGATAATAGATATTAA

## **FIGURE 90**

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVVDYVTVRKDAYMFWWLYYATNSC  
KNFSELPLVMWLQGGPGSSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPFVGTGFSY  
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR  
GTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNVKGLYRE  
ATELWGKAEMII EQNTDGVNFYNI LTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS  
QLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL  
IVDTMGQEAWRVKLKWPELPKFSQLKWKALYSDPKSLETSAFVKS YKNLAFYWILKAGHMVP  
SDQGDMA LKMMRLVTQQE

### **Signal sequence:**

amino acids 1-25

### **N-glycosylation site.**

amino acids 64-68, 126-130, 362-366

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 101-105

### **Casein kinase II phosphorylation site.**

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

### **N-myristoylation site.**

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,  
187-193, 195-201, 331-337, 332-338, 360-366

## FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGGGGCGCTGCTGCTGGCGTGCTGCTGGCTC  
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCGTATCAGGACCATGCGGCCGA  
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCA  
GGGGAGCCTGCGCCTGTGGGATTCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG  
CACTCACGGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG  
GTCCAGTTTGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCCTACTACACCCG  
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAAATCACCCCTATGACATTG  
CCTTGGTGAAGCTGTCTGCACCTGTGCACCTACACTAAACACATCCAGCCCATCTGTCTCCAG  
GCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA  
AGAGGATGAGGCACTGCCATCTCCCCACACCTCCAGGAAGTTCAGGTGCGCCATCATAAACA  
ACTCTATGTGAACCACCTCTTCTCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG  
GTTTGTGCTGGCAACGCCCAAGGCGGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCCCTT  
GGCCTGTAAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG  
GTCGGCCCCAATCGGCCCGGTGTCTACACCAATATCAGCCACCACCTTTGAGTGGATCCAGAAG  
CTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGGCCACTACTCTTTTCCCTCT  
TCTCTGGGCTCTCCCACTCCTGGGGCCGGTTGAGCCCTACCTGAGCCCATGCAGCCTGGGGC  
CACTGCCAAGTCAGGCCCTGGTTCTTCTGTCTTGTGTTGGTAATAAACACATTCCAGTTGA  
TGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 92**

MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAE LGRWPWQGSRLRW  
DSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSN I  
YLSPRYLGNSPYDIALVKLSAPVITYTKHIQFICLQASTFEFENRTDCWVTGWGYIKEDEALP  
SPHTLQEVQVAIINNSMCNHLFLKYSFRKDI FGDMVCAGNAQGGKDACFGDSSGGPLACNKNG  
LWYQIGVVSWGVGGRPNRPGVYTNISHHFEWIKLMAQSGMSQPDPSWPLLFFPLLWALPL  
LGPV

### **Signal sequence:**

amino acids 1-18

### **N-glycosylation site.**

amino acids 167-171, 200-204, 273-277

### **Casein kinase II phosphorylation site.**

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

### **N-myristoylation site.**

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,  
259-265, 269-275

### **Amidation site.**

amino acids 33-37

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 252-263,

### **Serine proteases, trypsin family, histidine active site.**

amino acids 78-84



## **FIGURE 94**

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSITFALRQQNVERLS  
ELVQAVSDPSSPOYGKYLTLNVADLVRPSPLTLHTVQKWLLAAGAQQCHSVITQDFTLCWL  
SIRQAELLPLGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGHLRFPPTSSLRQRP  
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG  
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLSAGANISTWVYSSPGRHEGQEPFLQWLML  
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH  
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP  
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG  
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPWDVPTGWGTPTSQLC

### **Signal sequence:**

amino acids 1-16

### **N-glycosylation site.**

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

### **Glycosaminoglycan attachment site.**

amino acids 361-365, 408-412, 538-542

### **Casein kinase II phosphorylation site.**

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

### **N-myristoylation site.**

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,  
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,  
521-527, 533-539, 549-555

## FIGURE 95

GCCGCGCGCTCTCTCCCGCGCCACACCTGTCTGAGCGGCGCAGCGAGCCGCGGCCCGGGC  
GGGCTGCTCGGCGCGGAACAGTGCTCGGCATGGCAGGGATTCCAGGGCTCCTCTTCTCTCTC  
TTCTTTTCTGCTCTGTGCTGTTGGGCAAGTGAGCCCTTACAGTGCCCTCGAAACCCACTTG  
GCCTGCATACCGCTCCTGTGCTCTTGCCCCAGTCTACCCTCAATTTAGCCAAGCCAGACT  
TTGGAGCCGAAGCCAAATTAGAAGTATCTTCTTCATGTGACCCAGTGTCATAAGGGAACT  
CCACTGCCCACTTACGAAGAGGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG  
CAGCCGCACAGAGACGCAGGTGGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCCAAC  
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTTATGGCTATGACAGC  
AGGTTTCAGCATTTTTGGGAAGGACTTCCTGCTCAACTACCCTTTCTCAACATCAGTGAAGTT  
ATCCACGGGCTGCACCGGCACCTGGTGGCAGAGAAGCATGTCTCACAGCTGCCCACTGCA  
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAAGCTTCGAGTGGGCTTCCTAAAGCCC  
AAGTTTAAAGATGGTGGTGCAGGGGCCAACGACTCCACTTCAGCCATGCCGAGCAGATGAA  
ATTTAGTGGATCGGGTGAAACGCACCCATGTGCCCAAGGGTTGGATCAAGGGCAATGCCA  
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAAGCTCAAAAAGCCCCACAAGAGAAAA  
TTTATGAAGATTGGGGTGAGCCCTCCTGCTAAGCAGCTGCCAGGGGGCAGAATTCACCTCTC  
TGTTTATGACAATGACCGACCAGGCAATTTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA  
CCTATGACTTGCTCTACCAGCAATGCGATGCCCAGCCAGGGGCCAGCGGTCTGGGGTCTAT  
GTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGGAGCGAAAAATTATTGGCATTTTTTCAGG  
GCACCAGTGGGTGGACATGAATGGTCCCCACAGGATTTCAACGTGGCTGTCAGAATCACTC  
CTCTCAAATATGCCAGATTTGCTATTGGATTAAAGGAACTACCTGGATTGTAGGGAGGGG  
TGACACAGTGTCCCTCCTGGCAGCAATTAAGGGTCTTCATGTCTTATTTTAGGAGAGGCC  
AAATTGTTTTTTGTCAATTGGCGTGACACCGTGTGTGTGTGTGTGTGTGTGTGAAGGTGT  
CTTATAATCTTTTACCTATTTCTTACAATTGCAAGATGACTGGCTTTACTATTTGAAAACGTG  
GTTTGTGTATCATATCATATATCATTTAAGCAGTTTGAAGGCATACCTTTGCATAGAAATAA  
AAAAAATACTGATTTGGGGCAATGAGGAATATTTGACAATTAAGTTAATCTTCACGTTTTTG  
CAAACCTTGATTTTTATTTTCATCTGAACCTTGTTTCAAAGATTTATATTAAATATTTGGCATA  
CAAGAGATATGAAAAAAAAAAAAAA

## **FIGURE 96**

MAGIPGLLFLFLFLLCAVGQVSPYSAPWKPTWPAAYRLPVVLPQSTLNLAKPDFGAEAKLEVS  
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGSSGKS  
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKG  
TQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA  
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCD  
AQPASGSGSVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYW  
IKGNYLDCREG

### **Signal sequence:**

amino acids 1-19

### **N-glycosylation site.**

amino acids 93-97, 207-211

### **Glycosaminoglycan attachment site.**

amino acids 109-113, 316-320

### **Casein kinase II phosphorylation site.**

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

### **N-myristoylation site.**

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

### **Serine proteases, trypsin family, histidine active site.**

amino acids 171-177



## FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCCGCCCCACCAGCCATGGTGGTTT  
CTGGAGCGCCCCCAGCCCTGGGTGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG  
GCGTCGACAGCCATCTCAATGCGGCCAGGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCA  
GCAGCTGAACCGGGTTGTGGGCGGCAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA  
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC  
ACTGCTGCCCACTGTTTCAAGGACAACCTGAACAAACCATACTGTTCTCTGTGCTGCTGGG  
GGCCTGGCAGCTGGGGAACCTGGCTCTCGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC  
CCCACCTGTGTATTCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCTCGAG  
CGCTCCATACAGTTCTCAGAGCGGGTCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT  
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCCTTGC  
CCCACCTCAGACCCTGCAGAAGCTGAAGGTTCCCTATCATCGACTCGGAAGTCTGCAGCCAT  
CTGTACTGGCGGGGAGCAGGACAGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTT  
GGAGGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCCCTCATGTGCCAGGTGGACG  
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCC  
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA  
GCTCCGCGGGCGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG  
CCGCGCGCTCCTTAGGGGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA  
TCTGGATCTGGATCTGCGGCGGCCTCGGGCGGTTTCCCCCGCGTAAATAGGCTCATCTACC  
TCTACCTCTGGGGCCCCGACGGCTGCTGCGGAAAGGAAACCCCTCCCGACCCGCCCCGAC  
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCGGCCAACGGCCTCATGTCCCCGCCCCAC  
GACTTCCGGCCCCCCCCGGGCCCGCAGCGCTTTTGTGTATATAAATGTTAATGATTTTAT  
AGGTATTTGTAAACCTGCCCCACATATCTTATTTATTCCTCCAATTTCAATAAATTATTATT  
CTCCAAAAA

## **FIGURE 98**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318  
><subunit 1 of 1, 317 aa, 1 stop  
><MW: 33732, pI: 7.90, NX(S/T): 1  
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAAIRIPVPPACGKPKQQLNRVVGGEDSTDSEWP  
WIVSIQKNGTHHCAGSLTTSRWVITAACHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVA  
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPNTHCWISGWGSIQDG  
VPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPIEDMLCAGYLEGERDACLGDSGGPLMC  
QVDGAWLLAGIISWGECAERNRPGVYISLSAHRWSVEKIVQGVQLRGAQGGGALRAPSQG  
SGAAARS

### **Signal sequence:**

amino acids 1-32

### **N-glycosylation site.**

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

### **Glycosaminoglycan attachment site.**

amino acids 826-830

### **Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

### **Tyrosine kinase phosphorylation site.**

amino acids 607-615

### **N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879



## **FIGURE 100**

MHGSCSFLMLLLPLLLLLLVATTGFPVGALTDEEKRLMVELHNLRYAQVSPITASDMLHMRWDEE  
LAAPAKAYARQCVVGHNKERGRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ  
MCGHYTQVVWAKTERIGCGSHFCEKLGVEETNIELLCVNYEPPGNVKGKRPYQEGTPCSQC  
PSGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSFRAATEASDSRKMGTPSSSLATGIPAFVLVTEV  
SGSLATKALPAVETQAPTSLATKDPSPMATEAPPCVTTTEVPSILAAHSLPSLDEEPVTFPKS  
THVPIPKSADKVTDKTKVPSRSPENSIDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS  
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSSLPGAEGPDKPSV  
SGLNSGPGHVWGPLLGLLLLLPLVLGIF

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

**Glycosaminoglycan attachment site.**

amino acids 439-443

**Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

**N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,  
250-256

**Amidation site.**

amino acids 82-86, 172-176

**Peroxidases proximal heme-ligand signature.**

amino acids 287-298

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

Figure 10.10

GTAACTCGAAGTCAGGCTCTTTCATTTTGGGAGGCCCTTCACAGAAATTCGGTCAATCTTCCACATGTTATGCTGGGACCAT  
ACTCTCTGTGTGTCCTCTCTCTCTCTCTCTCTTTCATCATACAGACCGGACTTAAGTCACACAGATATCTTCAT  
CAGGSCAAGTTCCTCAGCGACCTCTTCAAAGCCTCTCGAGAACTGAAACTGAAACAGATATGATTTGGAGACCATCC  
AAATCTGGGACCGAGTCTCGGCAAAATTTACACTTCTCTGCTCTGGCTGGAACAGAGTATTTGAAATCTCTCCCTGA  
ACATCTGGAAGAGTTTCAGTCCCTTGAAACTTTTGACCTTTAGCAGSCAACAAATTTTCAGAGCTCTCAAACTCAGT  
TCGCGCACTACAGCTCAAATATCTGATCTTCAACAGCAACCGAGTCACTATCCCACTCCCAAGATCTTTAAATCT  
TTTGGCCAAACATCATCTCTGTGTGTAAGCTGGAACGGAACGAGTCTCAGTATCCCACTCCCAAGATCTTTAAATCT  
GCCCACTCTGACCAACATCTCGAATGAAACCGAAACAGAGTAAAAATCTAGATGTAGCTGACATCTTCAATATCT  
TGTCTCTGAAAGTCTTGAAATGCAAAAGGATGGATTAACGAATCTATGAGTGGAGCTTTTGGGGGCTGGACCA  
TGAGTGAATTTTTCAGCTGGACCAATAACAACCTAACACAGAGTATACCAAGGCTGGCTTTTTCAGGCTCTGATGCTG  
CGAGGAAGTCTCATCTCAGCCAAATAGCCATCAACGAGTACGCCCTGAGTCTCTGGGGAGTCTCTCCAGAAGCTCAG  
TACTGCTGAACTTAACTTTCAATCATCTCAAGGTTTATGATGATTTCAAGTCTCTGCGCTTACAGTTCTTCAATAT  
ATCTGCACTTTGGGAAACAAGAGTCAGTAGTCATATGTCGATTGTCCTCCGGGGCTTCAGGTTTAAAGACTTT  
GGATCTGAAGAACCAATGAAATTTCTGCGCATCTTGAAGACATGAATGTGCTCTTTCTCTGGGGCTTGCAAACTGAG  
GCGAGTCAATCTCAAGGAAATTCGGATCGCTCTATTATCTAAAAAGGCTCTCAGTGGTTTGGATGTCTTGGAGCA  
TCTAGACCTGAGTGACAACGCAATCATGTCTTCAACGGCAATGCATTTTCAAAATGAAGAAATCTGCAACAACT  
GCATTTTAAATACATCAAGCTTTTGTGCGATCTGCGCATAAATGCTCCCAAGCGGGTGGGGGAAACAACTT  
TCAGAGCTTTGTAAATGCGAGTTGTGCCCATCTCAGCTCTGTAAGAGGAAGAAGCATTTTGGCTGTAGGCCATGA  
TGCTCTTTGTGTGTAGTATTTTCCAAACCCAGATCAGCTGACGCGAAGAAACAGTCTGCGCAATTAAGAGTTC  
CAATTTGAGTTTTCATCTGCTCAGCTCGCCACGACGAGTGATTTCCCAATAGCTTTTGTCTGGAAAGAAACAACTGA  
ACTACTGCAATGATGTCGATGAAGAAATATGCAACCTCCGGGCCAAGGTGGCGAGGTGATGAGTATAGCAATGCA  
CATCTCTCGGCTCGCGAGGTGGAATTTCCGATGAGGGGAAATATCAGTGTGCTCATCTCAATCACTTTTGGTCT  
ATCTCATCTCTGTCAGAAAGCAAGCTTAGTAGAATATGCTCTCCCTCATCAAGAACCCCTAGATCTCACATCT  
CCGAGCTGGGGCGATGCGACGCTCTGGAGTGTGCTCTGTGGGGCAACCGGCCCTCAGATAGCTCGGACAGATGAG  
GGGGGCAACAGACTCCAGCTGCAACGGGAGAGCACTCATGTGATGTCGCGAGGATGACGTGTTCTTTATCGT  
GGATGTGAAGATGAGGACATGTGGGTTATACAGCTGCGACAGCTCAGAACAGTGTGAGGAAAGTTTTCAGCAATGCA  
AACTCTGACTGTCTCTAGAAACCACTCATTTTTCGCGCCATCTGTGTGACCGCACTGTAAACAAGGGAAGAACGCA  
CGTCTCAACAGTGCATTTGCTGGAGGAGCCCTCCCTCCATTAAGTATGTCGACAAAGATGATAGCCCTATGGTGA  
AACCGAGAGGACATTTTTCGACAGAGCAATCTGCTTGTATTTGTGGAATCAGATGTCAAGTATGCTCGGGTAA  
ATACACATGTGAGATGTCTAACACCTTGCACTGAGAGAGGAAAGCACTGCGCCTCAGTGTGCTCCCATCTCAAC  
CTGCGCATCTCCCTCAGAGTACGCCCATCTGCTAGACAGTACAGGATGGGCGACTGTGGGTGTGCTGATCATGATCA  
CGTGGTTGTGCTGTGTGGGGACGCTCATCTGTGTGGGTGTGCTCATATACACCAAGCGCGAGGAATGAGAA  
TGTGCACTTTACCAACAGAGTACAGCACTTTGCCACAGATATCTTAGTATTTGTCTCATCGGGAACGCTTT  
AGCTCAGAGGACAGATAGGTAGCTGTCTTCAAGAAATGGAGGACCAACAGCTTTGTCACTCTCAGTGTCTGGT  
ATTTTTTCTTACCACAGGTCAGTAGTGGGACCTGCCATTTAGCAATACAGTAGAGCTGATGTGGAGTCTGCA  
CAGATCTGTTCTCTTGTGCGTTTGTGGATCAGACCGCCCTATGTATTGGAGGGAAATGTGATAGGCTCAGA  
TCTTTTGAACAATATACATACAGGTGTGCACTCTGACCAACAGAGCTTTTAAATGGAACAATAGAGCCGATGT  
CATTAAGAAAGAAAGAGTGCTACCAGTCTCTCATCTCTCAGAAAGATCTGCGACAGCGCTTCAGTAAATATTA  
TGTGGCTCTCAGATGTGAGGAGGCTACTTTAACATAGTTACTTTCACAAAGAGGACTGGAAATGAAAAATCTGTG  
TCTAAAGAGCTCCTCTTAGATTTTAGTGTGAACATCAGAGCGAGCGCTCGGTGGCTCGAGTAACTCTTTCATGGG  
TAOCTTTGGAAAGGCTCTCAGAGACCTCACTCAGATGCTTATCAAGTCTTGGACAGCACTAGATTGTACGCTCAGG  
AAGAGCTCTTTTATTTGAAGCTCATTTCTCCAGACCTTGAGCTCTGAGGTCAGAGGAAGATGGGAAAGAAAGAG  
AGATTTTTCAGGAAGAAATCTCAATTTGACTTTTAAACAGACTTTAGAAATACAGACATCCAAATTTCTCAGTCT  
TTATGACTTTGGACACATAGACTGAAATGAGACCAAGGAAAGACTTTAAACATACTCTCAGTGAACCTTTTATTT  
AAGAGAGAGATCTCTATGTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAGTCTTTTATTTATCAGAT  
GAACCAAAATATCAAAAGATTTAGAAATTTTATATCTGGGAATGATGCTCATATAGAAATACCTTTTAAATACT  
TTTTTTAACTTTTGTGTATGCAAAAAGATCTACTGCTAAATTAATGATATAAGTATGATTTTATGTATTT  
TTATAATCGCGAGTCTCTTTTGTGAAATAGGTTATCAAGAGCTTTTAAATATACTCTGCTGTACCCATTTT  
TTAAATAGAGATTTACTCATTTATTTTGCACATATTTTAAATTAAGTTGTCAATTTGAA

## **FIGURE 102**

MVDVLLLFSLCLLPHISRDPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSA  
ITLLSLAGNRIVEILPEHLKEFQSLETLDDLSSNNISELQTAFPAQLKLYLYLNSNRVTSMEP  
GYFDNLANTLLVLKLNRRNRI SAIPPKMFKLPQLQHELNRRNKIKNVDGLTFQGLGALKSLKM  
QRNGVTKLMDGAFWGLSNMEILQLDHNNTLEITKGWLYGLLMLQELHLSQNAINRISPDWE  
FCQKLSLELDLTFNHLRLDDSSFLGLSLNLTLHIGNNRVSYIADCAFRGLSSSLKTLDLKNNE  
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSIKKAFTGLDALEHLDSLDAIMSLQGNAFSQ  
MKKLQQLHLNLTSSLLCDCQLKWL PQWVAENNFQSFVNASCAPQLLKGRSIFAVSPDGFVCD  
DFPKPQITVQPETQSAIKGSNL SFICSAASSSDSPMTFAWKDNDLHDAEMENYAHRAQG  
GEVMEYTTILRLREVEFASGKYQCVISNHFSSYSVKAKLTVNMLPSFTKTPMDLIRAGA  
MARLECAAVGHPAPQIAWQKDGDTFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN  
SAGSISANATLTVLETPSFLRPLLDRTVTTKGETAVLQCIAGGSPPPKLNWTKDDSPLVVTER  
HFFAAGNQLLIIVDSVSDAGKYTCMSNTLGTGERGNVRLSVIPTPTCDSFQMTAPSLDDDG  
WATVGVVIIAVVCCVVGTSVLVWVVIYHTRRRNEDCSITNTDETNPADIPSYLSSQGTAD  
RQDGYVSSESGSHQFVTSSGAGFFLPQHDSSGTCCHIDNSSEADVEAATDLFLCPLFGSTGP  
MYLKGNVYGSDPFETYHTGCSDPDRTVLMDHYEPSYIKKKECYPCHSPSEESCERSFSNISW  
PSHVRKLNLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA  
YSSFGQPSDCQPPAFYLKAHSSPDLDSGSEEDGKERTDFQEENHICTFKQTLNRYRTPNFQS  
YDLDT

### **Signal sequence:**

amino acids 1-19

### **Transmembrane domain:**

amino acids 746-765

### **N-glycosylation site.**

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

### **Glycosaminoglycan attachment site.**

amino acids 826-830

### **Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

### **Tyrosine kinase phosphorylation site.**

amino acids 607-615

### **N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

# FIGURE 103

GGGGAGAGGAATGTACCATGTAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTGGGTGCCTTGCAAAAATG  
 AAGGATGCAGGACCGAGCTTTTCCTCGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGAAC  
 GAAGCTTTTTCTGTGAGCCCTGGATCTTAAACACAAATGTGTATATGTGCACACAGGAGGCAATTCAGAATGAA  
 TAAACAGAGATTAGACCCCGGGGGTGTGTGTCTTGACATAAATAAATAATCTTAAAGCAGCTGTTCCCTCC  
 CCACCCCCAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCACAAAGAAAAAGTATGTTTCATTTTTCTC  
 TATAAAGGAGAACTGAGCCACAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAAAGAACT  
 GGTGTGGTGGTGTTTTTCTTTCTTTTTGAATTTCCCAAGAGGAGAGGAAATTAATAATACATCTGCAAGAAAA  
 TTTGAGAGAGAAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACAGCAGAGACACAGTTGGA  
 TTTGTGCTGTATTGTGACTAAATTTGACGGATAATTGCAAGTTGGATTTTCTTCATCAACCTCTTTTTTAAAT  
 TTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTGTCTTAAACACCTGGATTTCATCTGGATGTTGCT  
 GTGATCAGTCTGAAATCAACTGTTTGAATTTCCAGAAGGACCAACACCCAGATAAATTAATGAATGTGAACAAGAT  
 GACCTTACATCCACAGCAGATAATGATAGGTCCTAGGTTTAAACAGGGCCCTAATTGACCCCTGCTTGTGGTGT  
 GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGGCGGGCTCAGACCTGCCCTTCTGTGTGCTCCTGCAGCAA  
 CCAGTTCCAGCAAGGTGATTTGTGTTCCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCAACACACGGCT  
 GCTGAACCTCCATGAGAACCAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGGCACTTGGAAATCCT  
 ACAGTTGAGTAGGAACCATACAGAACCATGAAATTTGGGGCTTTCATGTGTGCGCGAACCTCAACACTCTGGA  
 ACTCTTTGACAACTCCTTAACTACATCCCGAATGGAGCTTTGTATATCTGTCTAAAGTGAAGGAGCTGTGGTT  
 GCGAAACCAACCCCATTTGAAAGCATCCCTTCTATGCTTTTAAACAGAAATTCCTTTCTTGGCGCGCATAGACTTAGG  
 GGAATTTGAAAAGACTTTTATACATCTCAGAAGGTGCCCTTGAAGGCTGTGTCCAATTTGAGGTATTGAACTTGC  
 CATGTGCAACCTTCCGGGAATCCCTAACCTCACACCGCTCTATAAACTAGATGAGCTGGATCTTTTGGGAATCA  
 TTTATCTGCCATCAGGCTGGCTCTTTCCAGGGTTTGTATGCACTTCAAAGACTGTGGATGATACAGTCCAGTCA  
 TAACTGTGACATCTGTGGCTCAGCTGGTGGATAAAGACATGGCCCCCTCGAACACAGCTTGTGTGTGCCCGTGT  
 TAACTCTCTCCCAATCTAAAGGGGAGGTACATTGAGAGAGCTCGACCGAGAATTAATCTACATGCTATGCTCCGCT  
 GATTGTGGAGCCCCCTGCACCTCAATGTCACTGAAGGCATGGCAGCTGAGCTGAAATGTGGGGCTCCACATC  
 CCTGACATCTGTATCTTGGATTACTCCAAATGGAAACAGTCTAGACATGAGGGCGTACAAAGTGGCGATAGCTGT  
 GCTCAGTGATGTTACGTTAAATTTCACAAATGTAACTGTGCAAGATACAGGCTGTACACATGTATGGTGAGTAA  
 TTCCGTGTGGGAATACTACTGCTTCAGCCACCTCGAATGTTACTGCAGCAACCACTACTCTCTTCTTACTTTTC  
 AACCGTCAAGTAGAGACTATGGAACCGTCTCAGGATGAGGACCGACCAAGATACAAATGTGGGTCCCCTCC  
 AGTGGTGCAGTGGGAGACCAATGTGACCACTCTCTCAACCAACAGAGCAAGGTCGACAGAGAAAACTT  
 CACCATCCAGTGACTGATATAAACAGTGGGATCCCAAGAAATGATGAGGTCATGAAGACTCAAAAATCATAT  
 TGGGTGTTTTTGTGGCCATCACTCATGGCTGCAGTGATGTGTCATTTCTACAAGATGAGGAAGCAGCACC  
 TCGGCAAAACCATCACGCCCCAACAGGACTGTTGAAATTAATATGTGGATGATGAGATTACGGGAGACACAC  
 CATGGAAAGCCACTGCGCCATGCTGTCTGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTT  
 CACACACACAAACAGTTAAACAATAATTAATAACACAGTTCAAGTCAAGAACCGTTATTGATCCGAATGAA  
 CTCTAAAGCAATGTACAAGAGACTCAAATCAAACATTTACAGAGTTACAAAAAACCAACATCAAAAAA  
 GACAGTTTTATTAAAAATGACACAAATGACTGGGCTAAATCTACTGTTTCAAAAAAGTGTCTTTCAAAAAAACAA  
 AAAAGAAAAGAAATTTATTATTAAAAATCTATTGTGATCTAAAGCAGACAAAA

03000000-070000

## **FIGURE 104**

MLNKMTLHPQQIMIGPRFNRALFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVIC  
VRKNLREVDPDGISTNTRLLNLHENQIQIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA  
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS  
YISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL  
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNCDIL  
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE  
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTNLNFTNVTVQDTGMYTCMVNSVGN  
TTASATLNVTAATTPFSYFSTVTVTETMEPSQDEARTDNNVGPTPVVDWETTNTTSLTPQ  
STRSTEKTFTTIPVTDINSIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN  
HHAPTRTVEIINVDEITGDTMPMESHLPMPAIEHEHLNHNYSYKSPFNHTTNTVNTINSIHS  
VHEPLLIRMNSKDNVQETQI

### **Signal sequence:**

amino acids 1-44

### **Transmembrane domain:**

amino acids 523-543

### **N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,  
442-446, 488-492, 606-610

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

### **Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

### **N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
391-397, 422-428, 433-439, 531-537



# FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTCGAGTTGGCAGTTCTTTTCGGTTTCCCTCGCTGTTTGGGGGCA  
TGAAAAGGGCTTCGCCCGCGGAGTAAAGAAGGAATTGACCCGGGACGCGCGAGGAGCGCGCACGCCGCG  
GAGGGCGGGCGTGACCTCTCGGCTGCGAAGTTTGTCCGCGGCCCGCGAGCGCGCGCTGGGAGCTTCGGGTAGA  
GACCTTAGGCGCGTGACCGCGATGAGCGCGCGCGAGCTCCGTCGCGCGCGCGGGGTGGGGGCTGCTGCTGTGTC  
GCGGTGCTGGGGCGCGCTGCGCCGGTCCGACAGCGCGCGTCCGCGGGAACTCTCGGGCAGCTCTTGGGGTAGCGCCG  
GAGCGCCCATCGGCCCATCTCTGCCGCTGCCCTGGGGACCTGCTGGAGTCGAGTCGTAAAGCGGCTAGCGCGCTCTT  
CCCGAGGACATCTCCGCTCTGGGTCGCTCGGCTGGAGTTAAAGTCACAACAGATTATCTTTTCATCAAGGCAAGTCC  
ATGAGCGACCTTCAAAGCCTTCGAGAAGTGAACCTGAAACAACAATGAATTTGGAGACCATCCAAATCTGGGACCA  
GTCTCGGCGAAATATACATCTCTCTCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAG  
TTTCAGTCCCTTGAACCTTTGGACCTTAGCAGCAACAATATTTAGAGCTTCAAATCTGCATTTTCAGCGCTTACAG  
CTCAAATATCTGTATCTCAACAGCAACCGAGTCAATCAATGGAACCTGGGATTTTGACAATTTGGCCAAACACA  
CTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCCAAGATGTTTAAATCTGCCCAACTGCA  
CATCTCGAATTTGAACCGAACAAGATTAAAAATGTAGATGGACTGACATTTCCAAGGCCCTTGGTCTCTGAAGCT  
CTGAAAATGCAAGAAATGGAGTAAACGAACTTATGAGTAGGAGCTTTTGGGGGCTGAGCAACATGGAATTTTG  
CAGCTGGACCAATAACAACCTTAACAGAGATTACCAAGGCTGGCTTTACGGCTTGTGATGCTGCAGGAACCTTCAT  
CTCAGCGAAAATGCCATCAACAGGATCAGCCCTGATGCTCGGGAGTTCTGCCAGAAGCTCAGTGAGCTGCACCTTA  
ACTTTCAATCACTATCAAGGTAGATTCAAGCTTCTCTGGCCTAAAGCTTACAAATACACTGAGCGACTGATACTC  
AACACAGAGTGTGAGTACATTGTCTGATGTTGCTCTTCGGGGGCTTCCAGTTTGAAGACTTTGGATCTGAAGAAC  
AATGAATTTCTCGACTATTTGAAGACATGAATGGTGCTTCTCTGGGCTTGACAACTGAGGCGACTGATATCTC  
CAAGGAATCGGATCCGTTCTATTTACTAAAAAGCCTTCACTGGTTTGGATGCTATTTGAGCATCTAGACCTTGAT  
GACACCAATCACTGTCTTTTCAAGGCAATGCAATTTTCAAGGCAATGCACTTGAAGACTGCAACATTTGCAATTAATA  
TCAAGCCTTTTGTGCGATTGCCAGCTTAAATGGCTCCCAAGTGGGTCGGGAAACAACATTTACAGACTTTGTA  
AATGCCAGTTGTGCCATCTCAGCTGCTTAAAGGAAGAAGCATTTTGTCTGTAGCCAGTGGGCTTTGTGTGT  
GATGATTTTCCAAACCCAGATCAGCGTTTACGCGAGAAACAGCTCGGCAATAAAGGTTTCCAAATCTGACTTTC  
ATCTGCTCAGCTCGCAGCAGCATGATTTCCCAATGACTTTTGCTTGAAAAAAGACATGAACACTGCAATGAT  
GCTGAAATGGAAAAATTTATGCACCTCTCGGGCCAAAGGTGGCGAGGTGATGGAGTATACCAACATCTTCGCGT  
CGCGAGGTGGAAATTTGCCAGTGGGGGAAATATCAGTGTGTCATCTCCAATCACTTTGGTTCATCTCACTCTGT  
AAAGCACTTTACAGTAATGAGTTTCCCTCATTACCAAGACCCCATGGATTTCAACATCCGAGCTCGGGCC  
ATGGCAGCCTTGGAGTGTGTGCTGTGTGGGGCACCCAGCCCCAGATAGCTGGCAGAGGATGGGGGCGCAGAC  
TTCCAGCTGCAACGGGAGAGACGATGCAATGTGATGCCGAGGATGACGTGTTCTTTATCGTGGATGTGAAGATA  
GAGGACATTTGGGTATACAGCTGCAAGCTCAGAACAGTGCAGGAAGTATTTACAGCAATGCAACTCTGACTGT  
CTAGAAAACCACTATCTTTGCGGCCACTGTGTGACCGAACTGTAAACCAAGGAGAAACAGCCGCTCTACAGTGC  
ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAGATGATAGCCCATTTGTTGTTAAACGAGAGGAC  
TTTTTTTTCAGCAGGCAATCAGCTTCTGATTATTGTGGAATCAGATGTGCAATGATGTGGGAAATACACATGTGAG  
ATGTCTAACACCTTTGGCACTGAGAGAGGAAACGTGCGCTCAGTGTGATCCCCATCTCAACCTCGCATCTCCCT  
CAGATGACAGCCCATCGTTAGACGATGACGGATGGGCCCATGTGGGTGTCGATCATAGACCGCTGCAATGTGAG  
GTGGTGGGCAGTCACTCGTGTGGGTGTCTATATACCAACAAGGCGGAGGAATGAAGATTGCAAGCATTACC  
AACACAGATGAGACCAACTGTGCGAGCAGATATTCCTAGTTATTGTCTCATCTCAGGAACTGTAGCTGACAGGCG  
GATGGGTACGTGCTTCAGAAAGTGAAGGCCACCAACAGTTTGTACATCTTCAGGTGCTGGATTTTTCTTACCA  
CAACATGACAGTAGTGGGACCTGCGCATATTGACATAGCAGTGAAGCTGATGTGGAGCTGCCACAGATCTGTTCT  
CTTTGTCGGTTTGGGATCGACAGGCCCTATGATTTGAAGGGAATGTGTATGGCTCAGATCCTTTTGAACA  
TATCATACAGGTTGGAGCTCTGACCCAGACTGTTTAAATGGACCATTTTAAATGGACCATTTGACATAAAGAAAG  
GAGTGCTACCAATGTTCTATCTCTCAGAAAGTCTCTGCGAACGGAGCTTCAGTAAATATATCTGTGCTTCAT  
GTGAGGAAGCTTCAATCACTAGTTATCTCAATGAAGGACCTGGAATGAAATATCTGTGCTAAACAGTCTC  
TCTTTAGATTTTGAAGTCAAATCGAGGCCAGCGTGGTGTGCTCTGAGTAAATCTTTTATGSGGTACCTTTGGA  
GCTCTCAGGAGACCTCACTAGATGCTTCAAGCTTTGGACAGCCATGATTTGAGCTGAGCAGAGAGCTTTTAT  
TTGAAGCTCATTTTCCCAAGCTTGGACTCTGGGTGAGGAAGATGGGAAGAAAGAGACAGATTTTCAGGA  
GAAATCAATTTTGTACCTTTTAAACGACTTTAGAAAACCTACAGGACTCCAAATTTTCACTTTATGATCTTGGAC  
ACATAGACTTGAATGAGACCAAGGAAAGCTTAAACATACCTCAAGTGAATTTTAAAGAGAGAGAT  
CTATAGTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAGTCTTTATATACAGATGAACCAATTTAC  
AAAAAGTTATGAAATTTTATACCTGGGAATGATGCTCATATAAGATACCTTTTAACTATTTTAACTTTG  
TTTTATGCAAAAGTATCTTACTCAAAATTAATGATATAATCATGATTTTATGTATTTTATATATGCGAGA  
TTTTCTTTTATGGAATGAGTTACTAAAGCATTTTAAATAATACCTGCCCTGTACCATTTTTTAAATAGAGTT  
ACCTCATTATATTTTGACATATATTTAATAAATGTGCTAATTTGAAAAAAGGAAAAAAAAAAAAAAAAAAAA

## FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGRGELGQPSGVAAERPCPTTCRCLGDLDDCSR  
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNLEETIPNLGPVSANIT  
LLSLAGNRIVEITLPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY  
FDNLANTLLVLKLNRRNISAIIPKMKFLPQLQHLELNRNKIKNVDDLGLTFQGLGALKSLKMQR  
NGVTKLMDGAFWGLSNMEILQLDHNNTLITKGWLYGLLMLQELHLHLSQNAINRISPDWAFEC  
QKLSELDLTFNHLRLDDSSFLGLSLNLTLHIGNNRVSYIADCAFRGLSSSLKTLDLKNNIEIS  
WTIEDMNGAFSGLDKLRLLILQGNRIRISITTKAFTGLDALEHLDLSDNAIMSLQGNFASQMK  
KLQQLHLNNTSSLLCDCQLKWLPOWVAENNFQSFVNASCAPQLLKGRSIFAVSPDGFVCDFF  
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDKNELLHDAEMENYAHLRAQGG  
VMEYTTILRLREVEFASEGKYQCVISNHFSSSYSVAKLTVNMLPSFTKTPMDLTIIRAGAMA  
RLECAAVGHPPAQIAWQKDGTDFFAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA  
GSISANATLTVLETPSFLRPLLDRTVTVKGETAVLQCIAGGSPPPKLNWTKDSSPLVVTERHF  
FAAGNQLLIIVDSVDSDAGKYTCESNTLGTGRGNVRLSVIPTPTCDSPQMTAPSLDDDDGWA  
TVGVVIIAVVCCVGTSLVWVVIIYHTRRRNEDCSITNTDETNPADIPSYLSSQGTLDLRQ  
DGVVSSSGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY  
LKGNVYSGDPFETYHTGTCSPPDRTVLMDHYEPSYIKKCECYPSCSHPSSESCERSFSNISWPS  
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFFGKALRRPHLDAYS  
SFGQPSDCQPRAFYLLKAHSSPDLDSSGEEDGKERTDFQENHICTFKQTLNRYTPNFQSYDLDT

### **Signal sequence:**

amino acids 1-27

### **Transmembrane domain:**

amino acids 808-828

### **N-glycosylation site.**

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,  
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

### **Glycosaminoglycan attachment site.**

amino acids 886-890

### **Casein kinase II phosphorylation site.**

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,  
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,  
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,  
1073-1077, 1079-1083, 1081-1085

### **Tyrosine kinase phosphorylation site.**

amino acids 667-675

### **N-myristoylation site.**

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,  
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

### **Leucine zipper pattern.**

amino acids 58-80, 65-87

# FIGURE 107

CAAAACCTTGCCTCGCGGAGAGCGCCAGCTTGACTTGAATGGAAGGAGCCCCGAGCCCGCGGAGCGCAGCTGAGAC  
 TGGGGGAGCGCGCTTGCGCCCTGTGGGGCGCCGCTCGGCGCCGGGGCGCAGCAGGGAAGGGGAAGCTGTGGTCTGCC  
 CTGCTCCACAGAGGCGCCACTGGTGTGAACCGGGAGAGCCCTGGGTGGTCCCGTCCCTATCCCTCCTTTATATA  
 GAAACCTTCCACATCGGGAAGCAGCGCGCAGGAGGAGGCTCATGGTGAGCAAGGAGGCGCGCTGATCTGCAG  
 GCGCACAGCATTCGAGCTTTACAGATTTTACAGATACCAAATGGAAGGCGAGGAGGCGAGAACAAGCTGCTGGT  
 TCCATCAGCCCTGGCGCCCAGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCAGAGCGGGGTGCTGCG  
 TGCTCTGCTGCTGCTGCGGCCACAGCTGCACCTGGGACCTGTGCTTGCCGTGAGGGCCCGAGGATTTGGCCGAA  
 GTGGCGGCCACAGCCTGAGCCCCAGAGAGAACAATTTGCGGAGGAGGAGCGGTGCTGGTACTGAGCCCTGAGG  
 AGCCCGGGCTGGCCAGCGCGGTCAGCTGCCCGCAGACTGTGCTGTTCCAGGAGGGCGCTGTGGACTGTG  
 GCGGTATGACCTGCGTGAGTTCCCGGGGACCTGCTGAGCACAACCAACCATCTATCTCTGCAGAAACAACAGC  
 TGGAAAGATCTACCTCTGAGGAGCTCTCCGGCTGCACCGGCTGGAGACACTGAACCTGCAAAAACAACCGCTGA  
 CTTCCCGAGGGCTCCCAAGAGAAGCGTTTGAAGCATCTGAACCACTCAATTACCTGTACTTGGCCAAATAACAAGC  
 TGACCTTGGCACCOCCTTCTCCCAAAACGCTGATCAGTGTGACTTGTGTCGCAACATCTCTCGCCACGTCG  
 ATGGGCTCACCTTTGGCCAGAAGCCAACTTGAAGTCTGTGTACTGCAACAACAAGCTGGCAGAGCGCGGGC  
 TGCCGGAACAATGTTCAACGGCTCCAGCAACGTCGAGGTCTCTATCTGTGCAGCAACTCTCTCGCCACGTCG  
 CCAAGCACTGCGCCCTGCCCTGTACAAGCTGCACCTCAAGAAACAAGCTGGAGAAGATCCCCCGGGGGCT  
 TCAGCGAGCTGAGCAGCTGCGCAGCTATACCTGCAGAACAACACTACCTGACTGACGAGGGCTGGACAACGAGA  
 CCTTCTGGAAGCTCTCCAGCTGGAGTACTGTGATCTGTGCAGCAACAACCTGTCTCGGTCCCAGCTGGGCTGCG  
 CGCGCAGCCTGTGCTGCTGCACTTTGGAGAAGAACCGCATCCGAGCGTGGACGCGAATGTGCTGACCCCATCC  
 GCAGCTTGGAGTACTGCTGCTGCAAGCAACAGCTGCGGGAGCAGGCACTCACCACCTGGCTCTCCAGGGCC  
 TCAAGCGGTTCGACACGCTGCACCTGTATCAACAACGCGCTGGAGCGCGTGCACGCTGGCTGCGCGCGGTGCG  
 GCACCTCATGATCTGCACAACAGCATCAGGCATTTGGCCGCGAAGACTTTGCCACCACTACTTCTCTGGAGG  
 AGCTCAACCTCAGCTACAACCGCATCACAGCCCAAGGTGCACCGCGAGCGCTTCCGCAAGCTGCGCCTGTCG  
 GCTCGCTGGAGCTGTGCGGACACCGGCTGCACACGCTGCCACTGGGTGCTCTGAAATGTGCATGTGCTGAAGG  
 TCAAGCGCAATGAGCTGGTGCTTTGGCAGAGGGGCGCTGGCGGGCATGGCTCAGCTCGGTGAGCTGTACCTCA  
 CCAGCAACCGACTGCGCAGCCGAGCCCTGGGCGCCCGTGCCTGGGTGAGCTCCGCCATCTGCAGCTGTGGACA  
 TCGCCGGGAATCAGCTCACAGAGATCCCGGAGGGGCTCCCGAGTCACTTGAGTACCTGTACTCTGCAGAACACA  
 AGATTAGTGGCTGCCCGCAATGCCCTCGACTCCAAGCCCACTCAAGGGGATCTTCTCAGGTTTAAAGCAAGC  
 TGGCTGTGGGCTCCGTGGTGGACAGTGCTTCCGGAAGCTGAAGCACTGCAGGTCTTGGACATTGAAGGCACT  
 TAGAGTTTGGTGACATTTCCAAGGACCGTGCCGCTTGGGGAAGGAAAGGAGGAGGAGGAAAGGAGGAGGAGG  
 AGGAAGAGGAAACAAGATAGTGACAGGTGATGAGATGTGACCTAGGATGATGGACCGCGGACTCTTTTCTGTC  
 AGCACACGCTGTGTGCTGTGAGCCCCCACTCTGCCGTGCTCACACAGACACAACAGCTGCACACATGAGGCA  
 TCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTTCCACAGCGGTGTCACACGSCAGACACATGC  
 ACACACATCACCCCTCAAACACCCAGCTCAGCCACACACAACACTACCTCCAAACACCAAGTCTCTGTACAC  
 CCCCACCTACCGTGCCACGCGCTCTGAATCATGACGGGAAGGGTCTGCCCTTGCCCTGGCACAACACAGGCCACCA  
 TTCCCTCCCTGCTGACATGTGTATGCGTATGCATACACACACACACACATGACATGATGTGCGAA  
 CAGCCCTCCAAAGCTATGCCACAGACAGCTCTTGCCCGAGCCAGAATCAGCCATAGCAGCTCGCCCTGTGCGCT  
 CAGGACTGTGCGTCCGTCCCTGGAGAAGACACAAGGATATCCTGCTGTGGCGAGGTGCTGCGCACCTGCTGCGCT  
 GGAATCCCAAAAGCTGGCTTTATTTCTTTCCATCCTATGGGGACAGGACCTTCCAGGATCTGTGCGCTGCGC  
 TGGCCACCTCTGCTCCAGGTGCTGGGAGTCACTCTGCTAAGAGTCCCTCCCTGCCACCGCCCTGGCAGGACA  
 CAGGACTTTTCCATGGGCAAGCCAGTGGAGGACAGGATGGGAGAGCCCCCTGGGTGCTGCTGGGGCTTGGGG  
 CAGGAGTGAAGCAGAGTGTGGGGCTGGGCTGAGCCAGGAGGAGGACCCAGCTGCACCTGAGAGACACTTTT  
 GTTCTTCAGGCTGTGGGGAGGTTCGGGTGCTTTATTTTATTTCTTTCTAAGGAAAAAATGATAAAAT  
 CTCAAAGCTGATTTTCTGTATAGAAAACTAATAAAGCAATATCCCTATCCCTGCAAAAAATAA

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## **FIGURE 108**

MEGEEAEQPAWFHQPWRPGASDSAPPAGTMAQSRVLLLLLLLLLPPQLHLGPVLAVRAPGFGRS  
GGHSLSPREENEFAEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVDDCGGIDLREFPGDLP  
EHTNHLISLQNNQLEKIYPEELSRHLRLETNLQNNRLTSRGLPEKAFAHELTNLNLYLYLANNK  
LTLAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV  
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSRELYLQNNYLTDEGLDN  
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLLHSN  
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMLHNQITGIGREDFATTYF  
LEELNLSYNRITSQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALA  
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL  
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSSVDSAFRRLKHLQVLDIEGNLEFGDISK  
RGRLGKEKEEEEEEEEEEEETR

### **Signal sequence:**

amino acids 1-48

### **N-glycosylation site.**

amino acids 243-247, 310-314, 328-332, 439-443

### **Casein kinase II phosphorylation site.**

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

### **N-myristoylation site.**

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554

### **Leucine zipper pattern.**

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557

# FIGURE 109

GGGAGGGGGCTCCGGGCGCCGCGCAGCAGACCTGCTCCGGCCGCGCGCTCGCCGCTGTCTCTCCGGGAGCGGCAG  
CAGTAGCCCCGGGCGCGAGGGCTGGGGGTTCTCTGAGACTCTCAGAGGGGGCGCTCCCATCTCGCGCCCCACCACC  
CAACCTGTTCTCGCGCGCCACTCTGCGCTGCGCCCCAGGACCCGCTGCCAAATGATGATTTTCTCTGGCGCTGGT  
GCTGGTATCTCTCGCTCTACCTGCAGCGCGCGCGCGAGTTTCAGCGGAGGTTGGCCAGGCAAAATAGTGTCTATGAT  
TGGCCTATGTGCTTATGTGGGAGGATTGACTGCTGCTGGGCTGGGCTCGCCAGTCTTGGGACAGTGTCTCAGCC  
TGTGTGCGCAACACCATGCAAAATGTTGAATGTATCGGGCCAAACAAGTGCAGGTGTCTCTGGTTATGTCTGG  
AAAAACCTGTAACTCAAGATCTAAATGAGTGTGGCCTGAAGCCCCGGCCCTGTAAAGCACAGGTGCATGAACCTTA  
CGGCAGCTACAAGTGCTACTGTCTCAACGGATATATGCTCATGCCGGATGTTCTCTGCTCAAGTGCCCTGACCTG  
CTCCATGGCAAACTGTCAATGGCTGTGATGTTGTTAAAGGACAAATACGGTGCAGTGCCCATCCCTGGCCT  
GCACCTGGCTCTGATGGGAGGACCTGTGTAGATGTTGATGAATGTGTACAGGAAAGGCTCTCTGGCCTAGATT  
TAGGCAATGTCTCAACATTTTGGGAGCTACATCTGCAAGTGTCTATAAGGCTCTGATCTCATGTATTTGGAGG  
CAAAATATCAATGTCTAGATAGACGAATGCTCACTTGGTCAAGTGTACAGTGCAGCAGCTTGTCTGATGTTATATA  
CGTACGTGGGTCTCAAAAGTCAAAATGTTAAAGAGGATACCAAGGTGATGGACTGACTTGTGTGTATATCCAAA  
AGTTATGATGAACCTTCAGGTCCAATTCATGTACCAAGGGAAATGGTACCATTTTAAAGGGTGACACAGGAAA  
TAATAATTGGATTCTGATGTTGGAAGTACTTGGTGGCCTCCGAAGACACCATATATTTCCCTATCATTTACCAA  
CAGGCCCTACTTTAAAGCCAAACAAGACCTTACACCAAGGCCAAACCAATTTCTACTCCACCAACCCACCCACC  
CTGCTCAACAGAGCTCAGAACCTCTACCACTCAACCCAGAAAGGCCAAACCCGGACTGACAACTATAGC  
ACCAGCTCCAGTACACCTCCAGGAGGGATTACAGTTGACACAGGGTACAGACAGACCTTCAGAAACCCAGAGG  
AGATGTGTTTCAGTGTCTGGTACACAGTTGTAATTTTGACCATGCACTTTGTGGATGGATCAGGAGAGAAAGCAA  
TGACTTGCACTGGGAGCTCAATCAGGACCCAGCGTGGACAATATCTGACAGTGTCCGCGAGCCAAAGCCCCAGG  
GGGAAAAGCTCGACGCTTGGTGTACTCTCTCGGCCGCTCATGCAATCAGGCGAGCTTGTGCTCTGATTCAGGCA  
CAAGGTGACCGGGCTGCACTCTGGCACACTCCAGGTGTTGTGAGAAAACAGGTCCTCCAGCGGACAGCCCTGTG  
GGGAAGAAATGTTGGCCATGGCTGGAGGCAACACAGATCACTTTCGGAGGGGCTGACATCAAGAGCGAATACAA  
AAGATGAATTAAGGGTTGAAAAAAAGATCTATGATGGAAAATTAAGAGAACTGGGATTTATGAGCCTGGAGAG  
AGAAGACTGAGGGGCAACCATTTGATGTTTCTCAAGTATATGAAGGGTTGGCACAGAGAGGGTGGCGACCACTG  
TTCTCCATATGCACTAAGAAATAGAACAGAGGAAACTGGCTTAGACTAGATATAAGGGAGACTTTCTTGGCAGG  
GGCCATTTGTAAGATACTTATAAAAAAAGAGGTGTAATACTCAGATCTCTCTCTTTCTAAAAAATTAGA  
TAAAAAATTTGTCTATTTAAGATGTTTAAAGATGTTCTTACCAAGGAAAGTAAACAAATATAGAAATTTCCAAA  
AGATGTTTGTATCTCTAGTAGTATGCAAGTAAAAATCTTTAGAACTAAATAATTTGGACAAGGCTTAATTTTAGG  
CATTTCCCTCTTGACCTCTTAATGGAGAGGGATTGAAAGGGGAGAGCCACCAAAATCTGAGCTCACTGAAATA  
TCTCTCCCTTATGGCAATCTTAGCAGTATTAAGAAAAAAGGAAACTATTATCCAATGAGAGTATGATGGAC  
AGATATTTTAGTATCTCAGTAATGTCTTAGTGGCGGTGGTTTCAATGTTTCTTCAAGTAAAGGTATAAGCC  
TTTCAATTTGTTCAATGGATGTGTTTTCAGATTTTCTTTTAAAGAGATCCTTCAAGGAAACAGAGTTTCAAGAG  
ATTTTCATCGGGTGCAATCTCTCTGCTTCGTGTGTGACAAATGTTCTTGGCTGTGAGAAAGAGTGCCGCC  
ACACCGGCAGACCTTCTCTCACTCATCAGTATGATTCAGTTTCTCTTCAATTTGACTCTCCAGGTTCCAC  
AGAACAGTAATATTTTGAACAAATAGGTACAATAGAAGTCTTCTGTCATTTAACCTTGGTAAAGGCGGGCTGG  
AGGGGGAAAAATAATCATTAAGCCTTTGATTAACGGCAGAAATATAGGCTGTAGATCCATTTTAAATGGGTTTCAT  
TCTTTTATGTCATATAACTGCACAGCTGAAGATGAAAGGGGAAAAATAATGAAATTTTCACTTGTGATGCCAA  
TGATACATTCGACTAACTGATGGAAGAGTTATCCAAGTACTGTATAACATCTTGTATTATTATTAATGTTT  
CTAAAAATAAAATGTTAGTGGTTTTCCTAATGGCTTAATAAAACAATATTTGTAAATAAAACACTGTTAGTAA

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## **FIGURE 110**

MDFLLLALVLVSSSLYLQAAAEFDGRWRPQIVSSIGLCRYGGRIDCCGWARQSWGQCQPVCQP  
RCKHGEICIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD  
GSCSSALTCSMANCQYGC DVVKGQIRQCPSPLHLAPDGRTCV DVDECATGRASCPFRQC  
VNTFGSYICKCHKGF DLMYIGGKYQCHDIDEC SLGQYQCSSFARCYNV RGSYKCKCKEGYQG  
DGLTCVYIPKVMIBPSGPIHV PKNGTILKGD TGNNNWI PDVGSTWWPPKTPYIPPIITNRP  
TSKPTTRPTPKPTPIPTPPPPPLPTELRTPLPPTTPERPTTGLTTIAPAASTPPGGITVDN  
RVQTD PQKPRGDVFSVLVHSCNFDHGLCGWIREKDN DLHWEPIRDPAGGQYLT VSAAKAPGG  
KAARLVLP LGRLMHSGDLCLSF RHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI  
TLRGADIKSESQR

### **Signal sequence:**

amino acids 1-17

### **N-glycosylation site.**

amino acids 273-277

### **Casein kinase II phosphorylation site.**

amino acids 166-170, 345-349

### **Tyrosine kinase phosphorylation site.**

amino acids 199-206

### **N-myristoylation site.**

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,  
421-427, 433-439, 462-468, 476-482

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

### **Cell attachment sequence.**

amino acids 382-385

### **EGF-like domain cysteine pattern signature.**

amino acids 75-87

# FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTTGCCCTTTAGATTGTGA  
**AATG**TGGCTCAAGGCTTTCACAACTTTCCTTTCTTTTGCAACAGGTGCTTGCTCGGGGCTGA  
 AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTTACCTACCCGTC  
 CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCA  
 CACAATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCTTGACTTGGAATACC  
 AACACAAGTTCACCATGATGCCACCCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCCT  
 GATGAAGGCAATTACATCGTGAAGGTCAACATTGAGGAAATGGAAGTCTATCTGCCAGTCA  
 GAAGATACAAGTCAAGGTTGATGATCCTGTCAAAAGCCAGTGGTGCAGATTATCCTCCCT  
 CTGGGCTGTGGAGTATGTGGGGAACATGACCTGACATGCCATGTGGAAGGGGGCACTCGG  
 CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCAACACAGCTCCACCTACTCCTTTTC  
 TCCCCAAAACAATACCCCTTCAATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT  
 GCCTGGTGAGGAACCCCTGTCAAGTGAATGGAAAGTGATATCATTATGCCCATCATATATTAT  
 GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAAGTAGGGGAAGTGTCTACTGT  
 TGACCTTGGAGAGGCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT  
 CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAGCATGGGCCCTCGTTAGAAATT  
 GCATCTGAGAAAGTAGCCAGAACAAATGGACTATGTGTGCTGTGCTTACAACAACATAAC  
 CGGCAGGCAAGATGAAACTCATTTACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG  
 CACAGAAAGGAAAAATCATTTGTACCTTTAGCAAGTATAACTGGAATATCACTATTTTGTATT  
 ATATCCATGTGTCTTCTTCTTCTTATGGAAAAATATCAACCTTCAAAAGTTATAAAAAAGAA  
 ACTAGAAGGCAGGCCAGAAACAGAAATACAGGAAAGCTCAAACATTTTCAGGCCATGAAGATG  
 CTCTGGATGACTTCGGAATATATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTCACAG  
 ATTTCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGGCAAGATTGACAGTACAGT  
 GTATGAAGTTATTGACGACATCCCTGCCAGCAGCAAGACCATCCAGAGT**GAA**CTTTTCAATGG  
 GCTAAACAGTACATTGAGTGAAATTTCTGAAGAAACATTTTAAGGAAAAACAGTGGAAGT  
 ATATTAACTGGAATCAGTGAAAGAACAGGACCAACACCTCTTACTCATTTATTCCTTTACA  
 TGCAGAATAGAGGCATTATGCAAAATTGAACTGCAGGTTTTTCAGCATATACACAAATGTCTT  
 GTGCCACAGAAAAACATGTTGGGGAAATATTCCTCAGTGGAGAGTCTGTTCTCATGCTGACGG  
 GGAGAACGAAAGTGACAGGGGTTTTCTCATAAGTTTTGTATGAAATATCTCTACAAACCTCA  
 ATTAGTTCTACTCTACACTTTCACTATCATCAACACTGAGACTATCCTGTCTCACCCTACAAA  
 TGTGGAAGCTTTTCAATTGTTTCGATTTTTCAGCAGACTTGTGTTTTTAAATTTTTTATAGTG  
 TTAAGAATGCTAAATTTATGTTTCAATTTTATTTCCAAATTTCTATCTTGTATTGTTACAA  
 CAAAGTAATAAGGATGGTTGTCAAAAAACAAACTATGCCTTCTCTTTTTTTTCAATCACC  
 AGTAGTATTTTTTGGAAGACTTGTGAACACTTAAGGAAATGACTATTAAGGTCTTATTTTTA  
 TTTTTTTCAAGGAAAGATGGATTCAATAAATTATTCGTTTTTGCTTTTAAAAA

## **FIGURE 112**

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH  
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQNGTLSASQ  
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNRPPVHTSSTYSFS  
PQNNTLHIAFPVKEDIGNYSCLVRNPFVSEMSDIIMP I I I Y G P Y G L Q V N S D K G L K V G E V F T V  
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT  
GRQDETHFTVIITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKKYQPYKVIKQK  
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRVSPASDCVSGQDLHSTV  
YEVIQHIIPAQQQDHPE

### **Signal sequence:**

amino acids 1-18

### **Transmembrane domain:**

amino acids 341-359

### **N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,  
276-280, 308-312

### **Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

### **Tyrosine kinase phosphorylation site.**

amino acids 272-280

### **N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,  
239-245

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18



## FIGURE 113

GCAAGCGCGGAAATGCGGCCCTCCGGGAGTCTTGCAGTTCCCTTGGCAGTCCCTGGTGTCTGTT  
GCTTTGGGGTGCTCCCTGGACGCACGGGCGGCGGAGCAACGTTTCGGTGCATCACGGACGAGA  
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAAATTTATGCCCGTGGTGCCCTGCT  
TGTCAAAATCTTCAACCGGAATGGGAAAGTTTTGCTGAATGGGAGAAGATCTTGAGGTTAA  
TATTGCGAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTTTATCATAACTGCTC  
TTCCTACTATTTTATCATTTGTAAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAAGGACTAAG  
AAGGACTTCATAAACTTTTATAAGTGATAAAGAGTGGAAAGATATTGAGCCCGTTTCATCATG  
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACCTCTTTCAGCTATCTATGTGGA  
TCAGGACGTCGCCATAACTACTTTATTTGAAGACCTTGGATTGTCAGTGTGGGGATCATATACT  
GTTTTTGCTTTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTTGGGC  
AGATTGCCCTTGTCTTCAAAAAGCGCAGACCACAGCCATACCCATACCTTCAAAAAAT  
TATTATCAGAATCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA  
GATGTTTCAGAAGAAGAAGCTGAAAGTAAAGAAGGAACAACAAAGACTTTCACAGAATGC  
CATAAGACAACGCTCTCTGGGTCCATCATTGGCCACAGATAAATCCTAGTTAAATTTTATAG  
TTATCTTAATATTATGATTTTGATAAAAAACAGAAGATTGATCATTTTGTTTGGTTTGAAGTG  
AACTGTGACTTTTTTGAATATTGCAGGGTTTCAGTCTAGATTGTCTATTAAATGAAGAGTCTA  
CATTACAGAACATAAAAGCACTAGGTATACAAGTTTGAATATGATTTAAGCACAGTATGATG  
GTTTAAATAGTTCTCTAATTTTTGAAAAATCGTGCCAAGCAATAAGATTTATGTATATTTGT  
TTAATAATAACCTATTTCAAGTCTGAGTTTTGAAAAATTACATTTCCCAAGTATTGCATTAT  
TGAGGTTATTAAGAAGATTATTTAGAGAAAAATATTTCTCATTTGATATAAATTTTCTCTG  
TTTCACTGTGTGAAAAAAGAGATATTTCCATAAATGGGAAGTTTGCCCATTTGCTCTCAAG  
AAATGTGTATTTCACTGACAATTTCTGGTCTTTTTAGAGGTATATCCAAAAATTTCTTGT  
ATTTTTAGGTTATGCAACTAATAAAAACTACCTTACATTAATTAATTACAGTTTTCTACACA  
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTTTAAGTTTCATGGTATTCTCTTGATTC  
CAACAAAGTTTGATTTTCTCTGTATTTTTCTTACTTACTTGGGTACATTTTTTATTTTT  
CAAATTTGGATGATAATTTCTTGGAAACATTTTTTATGTTTTAGTAAACAGTATTTTTTTGTT  
GTTTCAAACCTGAAGTTTACTGAGAGATCCATCAAATTGAACATCTGTTGTAATTTAAATTT  
TTGGCCACTTTTTTCAGATTTTACATCATTCTTGCTGAACTTCAACTTGAAATTTGTTTTTTT  
TTTCTTTTTGGATGTGAAGGTGAACATTTCTGATTTTTGTCTGATGTGAAAAAGCCTTGGTA  
TTTTACATTTTGAAAAATTCAAAGAAGCTTAATATAAAAGTTTGCATTCTACTCAGGAAAAAG  
CATCTTCTTGATATATGCTTAAATGTATTTTTTGTCCTCATATACAGAAAGTCTTAAATTGAT  
TTTACAGTCTGTAATGCTTGATGTTTTAAATAATAACATTTTTATATTTTTTAAAGACAA  
ACTTCTATATTATCCTGTGTCTTTCTTGACTGGTAATATTGTGTGGGATTTACAGGTA  
GTCAGTAGGATGGAACATTTTAGTGTATTTTACTCTTTAAAGAGCTAGATAATAGATGTTTT  
CACCTTAAAGAAGGGGAAAAATCATAAATACAATGAATCACTGACCATCTAGTAGTAGAC  
AATTTCTGTAATGTCCCTTCTTTCTAGGCTCTGTGTGCTGTGAATCCATTAGATTTACAG  
TATCGTAATATACAAGTTTCTTTTAAAGCCCTCTCCTTTAGAATTTAAATATTGTACCAT  
AAAGAGTTTGGATGTGTAATTTGTGATGTCCTTAGAAAAATATCCTAAGCACAAAATAACCT  
TTCTAACCACTTCATTAAGCTGAAAAA

## **FIGURE 114**

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL  
QPEWESFAEWGEDLEVNIKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI  
NFIISKWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL  
ATLFSGLLLGLCMIFVADCLCPSKRRRPQYPYPYPSKKLLSESAQPLKKVEEEQEAEDEEDVSE  
EEAESKEGTNKDFPFQNAIRQRS LGPSLATDKS

### **Signal sequence:**

amino acids 1-26

### **Transmembrane domain:**

amino acids 182-201

### **Casein kinase II phosphorylation site.**

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

### **Tyrosine kinase phosphorylation site.**

amino acids 107-115

### **N-myristoylation site.**

amino acids 20-26, 192-198

### **Amidation site.**

amino acids 25-29

## FIGURE 115

GCGAGTGTCCAGCTGCGGAGACCCGTGATAAATTCGTTAACTAATTCAACAAACGGGACCCTT  
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCGGATTTGGAAAGAGCGGG  
AAGGTCCTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGTCTGC  
ATTGCTGATGGCCTGGTTTGGTGTCTTGAGCTGTGTGCAGGCCGAATTCCTCACCTCTATTG  
GGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGAGTCTCTGAAAAGAGTACATC  
CTTGTGGAGGAAGCCAAAGCTTTCAGATTAAAGAGCTGGGCCAACAAATGGAAGCCCTTGAC  
TAGCAAGTCAGCTGTGTGCTGAGGGCTACTGGCTCACCTGTGTAATGCCTACAAACTGG  
TGAAGCGGCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA  
GCTTTTATCGCCAACTCTCTGTGCAGCGGACGTTCTTCCCCACTGATGAGGACGAGATAGG  
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAAATTTCCA  
GAGGGGAACCTTCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG  
GGCCGCTCGGCCTACAATGAAGGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCT  
AAAGCAGCTTGATGCCGGGGAGGAGGCCACCAACCAAGTCACAGGTGCTGGACTACCTCA  
GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTACCCGCCGCTGTCTC  
TCCCTTGACCCAAGCCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGA  
GGAAGAGAGAGAAAAACGTTAAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAGGGCA  
TCTATGAGAGGCTGTGGACTACCTGCCTGAGAGGGATGTTTTACGAGAGCCTCTGTCTGGGG  
GAGGGTGTCAAACCTGACACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCACCATGGCAA  
CAGGGCCCCACAGCTGCTCATTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACA  
TCGTCAAGTACTACGATGTCTGCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA  
CCTAAACTTGCACGAGCCACCGTTCTGTGATCCCAAGACAGGAGTCTCTCACTGTCTGCCAGCTA  
CCGGGTTTCAAAGCTCCTGGCTAGAGGAAGATGATGACCCGTGTTGTGGCCCGAGTAAATC  
GTCGGATGCAGCATATCACAGGTTAAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAAT  
TATGGAGTGGGAGGACAGTATGAACCCGACTTCGACTTCTCTAGGCGACCTTTTGACAGCGG  
CCTCAAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACTACATGATGATGTAGAAGCTG  
GTGGTGCCACCGTCTTCCCTGATCTGGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTG  
TTCGTGTAACAACCTCTTGCAGGCGGGGAAGGTGACTACCGAACAGACATGCTGCTGCCGCC  
TGTGCTTGTGGGCTGCAAGTGGGTCTCCAATAAGTGGTTCCATGAACGAGGACAGGAGTTCT  
TGAGACCTTGTGGATCAACAGAAGTTGACTGACATCCTTTTCTGTCTCTCCCTTCTCTGGTC  
CTTCAGCCCATGTCAACGTGCAGACACCTTTGTATGTTCTTTGTATGTTTCCATCAGGCT  
GATTTTGGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT  
GTGACTGAAGTCCCAGCCCTTCCATTGAGCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA  
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCCTTTGTACCTCAGGTGTT  
TTAGGTGTGAGATGTTTCACTGAACCAAGTTCTGATACCTTGTGTTTACATGTTTGTGTTTTAT  
GGCATTTCATCTATTGTGGCTTTACCAAAAAATAAAATGTCCCTACCAGAAAAA

## **FIGURE 116**

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEEKELVQSLKEYILVEEAKLSKIKSWA  
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDVLQDSAAGFIANLSVQRQFFP  
TDEDEIGAALKALMRLQDTYRLDPGTISRGE LPGTKYQAMLSVDDCFGMGRSAYNEGDDYYHTV  
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR  
YFEQLLEEEEREKTLTNQTEAELATPEGIYERPVVDYLPERDVYESLCRGEVVKLTPRRQKRLF  
CRYHHGNRAPQLLIAPFKEEEDWDSPHIVRYDVMSEDEIERIKEIAKPKLARATVRDPKTG  
VLTVASYRVSKSSWLEEDDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS  
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEGDYR  
TRHAACPVLVGCKWVSNKWFHERGQEFRLPCGSTEV

### **Signal sequence:**

amino acids 1-17

### **N-glycosylation site.**

amino acids 115-119, 264-268

### **Glycosaminoglycan attachment site.**

amino acids 490-494

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 477-481

### **Casein kinase II phosphorylation site.**

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,  
346-350, 365-369, 385-389, 457-461, 530-534

### **Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

### **N-myristoylation site.**

amino acids 14-20, 131-137, 171-177, 446-452

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 8-19

### **Leucine zipper pattern.**

amino acids 213-235

## FIGURE 117

GCAGTATTGAGTTTACTCTCCTCTCTTTTAGTGGAAGACAGACCATAATCCCAGTGTGAGTGAAATGATTGT  
 TTCATTATTACCGTTTTTGGCTGGGGGTTAGTTCGACACCTTCACAGTTGAAAGAGCAGGCAGAGGAGTTGTGA  
 AGACAGGACAATCTCTTTGGGGATGCTGGCTCGGAAGCCAGCGGGCTTGCTCTGTCTTTGGGCTCATTTGACCC  
 CAGGTTCTCTGGTTAAAACTGAAGCCCTACTACTGGCCTGGTGGCCATCAATCCATTGATCTCTGAGGCTGTGCC  
 CCTGGGGCACCCCTGGCAGGGCTACCACTAGCGACTGAGCTCCCTGTTGGCTCTGCTCGGGCCAGCGCTTC  
 CCTCATCTTAGGGCTGTCCTCTGGGGTGACGCTGAGCCTCCTGCGGGTTTCCTGGATCCAGGGGGAGGGAGAAG  
 ATCCCTGTGTCGAGGCTGTAGGGGAGCGAGGAGGGCCACAGAATCCAGATTCCGAGAGCTCGGCTAGACCAAAGTG  
 ATGAAGACTTCAACACCCCGGATTGTCCCCTACTACAGGGACCCCAACAAGCCCTACAGAAGGCTCTCAGGACTC  
 GGTACATCCAGACAGAGCTGGGCTCCGCTGAGCGGTTGCTGGTGGCTGCTTACCTCCCGAGCTTACACTGTCCA  
 CTTTGGCCGTGGCTGTGAACCTACGGTGGCCCATCACTCCCTCGGTTACTCTACTTCACTGGGCAGCGGGGGG  
 CCGGGCTCCACAGGGATGCAAGTGGTGTCTCATGGGATGAGCGGCCCGCTGGCTCATGTACAGAGCCCTGC  
 GCCACTTCAACACACTTTGGGGCCGACTACGACTGGTCTTTCATCATGACGGATGACACATATGTGACGGCCC  
 CCGGCTGGCAGCCCTTGCTGGCCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGGCAGAGGAGTTTCATTG  
 GCAGCGCGAGCAGGCCCGGTACTGTCTATGGGGCTTTGGCTACCTGTTGTGACGAGCTCTCTGCTTGTCTGTC  
 GGCCCATCTGGATGGCTGCGGAGGAGACATTTCAAGTCCCGCTCTGACAGTGGCTTGGACGCTGCTTCATTG  
 ACTCTCTGGGCTGCGGCTGTGCTCAGACACAGCGGCAGCAGTATCGCTCATTTGAACTGGCCAAAAATAGGG  
 ACCCTGAGAAGGAAGGAGCTCGGCTTCTCTGAGTGCCTTCGGCGTGACCCCTGTCTCCGAAGGTACCTCATGT  
 ACCGGCTCCACAAAGCTTCAGCGCTCTGGAGTTGGAGCGGGCTTACAGTGAATAAGAACACTGCAGGCTCAGA  
 TCCGGAACCTGACCGTGCTGACCCCGAAGGGAGGAGCGGCTGAGCTGGCCCGTTGGGCTCCCTGCTCTTTTCA  
 CACCACACTCTCGCTTTGAGGTGCTGGGCTGGGACTACTTACAGAGCAGCACACTTCTCTGTGACAGATGGG  
 CTCCTCAAGTGCCCACTACAGGGGGCTAGCAGGGCGGACGTGGGTGATGCGTTGGAGACTGCCTGGAGCAGCTCA  
 ATCGGCGCTATCAGCCCGGCTGCGCTTCCAGAAGCAGCGACTGCTCAACGGCTCATCGGCGCTTCAGCCAGCAG  
 GGGCATGGATACACCTTGACCTGTGTTGGAATGTGTGACACAGCGTGGGCACCGGCGGGCCTGGCTCGCA  
 GGGTCAGCCTGCTCGGCCACTGAGCCGGGTGGAATCCTACTATGCGCTATGTCACTGAGGCCACCCGAGTGC  
 AGCTGGTGTGCTCACTCCTGTGTGCTGAAGCTGCTCGAGCCCGGCTTTCCTCGAGGCGTTTGACGCAATGTCC  
 TGGAGCCACGAGAACATGCTATTCTCACCTGTGCTGGTCTACGGGCCACGAGAAGTGGCGTGGAGCTCCAG  
 ACCCATTTCTTGGGGTGAAGGCTGAGCAGCGGAGTTAGAGCGACGGTACCTCGGACAGGCTGGCTGGCTCG  
 CTGTGCGAGCAGAGGCCCTTCCAGGTGCGACTCATGGAGCTGGTCTCGAAGAAGCACCTGTGGACACTCTCT  
 TCTTCTTACCACCGTGTGGACAAGGCTGGGCCCGAAGTCTCTCAACCGCTGTGCGATGAATGCCATCTCTGGCT  
 GGCAGGCTTCTTTCCAGTGCATTTCCAGGAGTTCATCTGCTGCTGACCAACAGAGATCACCCCAAGGCCCC  
 CGGGGGCTGGCCCTGACCCCCCTCCCTCCTGGTGTGACCCCTCCCGGGGGGCTCTATAGGGGGGAGATTG  
 ACCGGCAGGCTTCTCGGGAGGGCTGCTTCAACAACGCTGACTACTGGCGGGCCGAGCCCGGCTGGCAGGTGAAC  
 TGGCAGGCACGGAAGAGGAGGAAGCCCTGGAGGGGCTGGAGGTAGTGAATTTCTCCGGTTCTCAGGCTCC  
 ACCTCTTTCCGGGCTTAGAGCCAGGGCTGGTGCAGAAGTTCTCCCTCGAGACTGCAGCCACGCTCAGTGAAG  
 AACTCTACACCGCTGCCGCTCAGCAACTGGAGGGGCTAGGGGGCGGTGCCAGCTGGCTATGGCTCTCTTTG  
 AGCAGGACAGGCCAATAGCACTTAGCCCGCTGGGGGCCCTAACTCATTAACCTTCTCTTTGTCTGCTCAGCC  
 CCAGGAAGGCCAAGCAAGATGTTGGACAGATAGAGAATTTGCTGTATTTTTAAATATGAAATGTTATTAA  
 ACATGTCTTCTGCC

## **FIGURE 118**

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQEGEDPCVEAVGERGGPQNPDSSRARLD  
QSDDEFKPRIVPYRDPNPKPYKKVLRTRYIQTELGSRRERLLVAVLTSRATLSTLAVAVNRTV  
AHHFPRLLYFTGQRGARAPAGMQVVS HGDERPANLMS ETLRHLH THFGADYD WFFIMQDDTY  
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG  
DILSARPD EWLGRCLIDSLGVGCVSQHQGQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE  
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLT VLTPEGEAGLSWFPVGLPAPFTPHSRFEV  
LGWDYFTEQHTFSCADGAPKCPLOGASRADVGDAL E TALEQLNRRYQPRLRFQQRLLNGYR  
RFDPARGMEYTLDLLL ECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVLP LL  
VAEAAAAPAFLEAFAANVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAAELERRYPG  
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLT TVWTRPGPEVLNRCRMNAISGWQAFPP  
VHFQEFNPALSPQRSPPGPPGAGDPDPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA  
RARLAGELAGQEEEEALEGLEVM DVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR  
CRLSNLEGLGGRAQLAMALFEQE QANST

### **Signal sequence:**

amino acids 1-15

### **Transmembrane domain:**

amino acids 489-507

### **N-glycosylation site.**

amino acids 121-125, 342-346

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

### **Casein kinase II phosphorylation site.**

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

### **Tyrosine kinase phosphorylation site.**

amino acids 736-743

### **N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-678

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

### **Cell attachment sequence.**

amino acids 247-250

## FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGGGCTGCGCTTTCTGTCCCCAAGCC  
GTTCTAGACGCGGGAATAATGCTTTCTGAAAGCAGCTCCTTTTGAAGGGTGTGATGCTTGG  
AAGCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA  
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAAATTCA  
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTCGAGTATACTGTATTATCCTTGTAAACC  
CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAACACTGTGACAAAGCAG  
AGTTCTTCAGTCTTGAAAAATGTTAAAGTGTGAGTCAATTAATATGGACACAAATGACATG  
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACCTG  
GTTCTTCTTGCACGCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTAA  
AAAAGGATCCATCAGACCTTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT  
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT  
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAAC  
AGCTAGCAGTTTGCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA  
AAAGATGTATTTAATACCAATCTGTTGGGCTTCTATTAAAGAGGCAATGACTTATCACCC  
CAACCAGGTAGTAGAAGGCTGTTGTTTTCAGATATGGCTGTACTTTTAAATGGACTGACTCAA  
ATCAGATGCATGTGATGATGTATGGGGTATACCGCCTTAGGGCATTGGGCATATTTTCAAT  
GATGCATTGGTTTTCTTACCTCCAATGGTTCTGACAATGACTGAAGAGTGGTAGAAAAGCG  
TGAATATGATCTTTGTATAGGACGTGTGTTGTCTATTATTGTAGTAGTAACATACATATCCAA  
TACAGCTGTATGTTTCTTTTCTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAG  
TCAGTAGTACATTTTAAATGAGGGTGGTTTTTTTCTTTAAACACATGAACATTGTAAATG  
TGTGGAAAGAAGTGTTTTAAAGAATAATAATTTTGCAAATAAACTATTAAATAAATATTATAT  
GTGATAAATTTCTAAATTATGAACATTAGAAATCTGTGGGACACATATTTTGTCTGATTGGTT  
AAAAAATTTTAAACAGGTCTTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT  
TGTGATTAAAGTAAACCTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTATGTCTCT  
AAGCCTCCCCAAGTTCCAATGGATTGTCCTTCTCAAAATGTACAACTAAGCAACTAAAGAAA  
ATTAAAGTGAAAGTTGAAAAAT

## **FIGURE 120**

MLSESSSFLKGVMGLSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME  
LSKSFVRVYCIILVVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRK  
AYKYAFDKYRDQYNWFFLARPTTFAIENLKYFLKKDPSQPFYLGHTIKSGDLEYVGMEGG  
IVLSVESMKRLNSLLNIPEKCEQGGMIWKISEDQLAVCLKYAGVFAENAEDADGKDVFNT  
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL  
PPNGSDND

### **Signal sequence:**

amino acids 1-33

### **N-glycosylation site.**

amino acids 121-125, 342-346

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

### **Casein kinase II phosphorylation site.**

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

### **Tyrosine kinase phosphorylation site.**

amino acids 736-743

### **N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-672

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

### **Cell attachment sequence.**

amino acids 247-250



Time	Temp	Time	Temp	Time	Temp	Time	Temp
0	25	10	25	20	25	30	25
10	25	20	25	30	25	40	25
20	25	30	25	40	25	50	25
30	25	40	25	50	25	60	25
40	25	50	25	60	25	70	25
50	25	60	25	70	25	80	25
60	25	70	25	80	25	90	25
70	25	80	25	90	25	100	25
80	25	90	25	100	25		
90	25	100	25				
100	25						

[illegible]

## **FIGURE 122**

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN  
FTELSYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALS LKNCSAMGAHLVVINSQEEQ  
EFLSYKKPKMREFFIGLSDQVVEGQWVDGTPLTKSLSFWDVGEFNNIATLED CATMRDSS  
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

### **Signal sequence:**

amino acids 1-42

### **N-glycosylation site.**

amino acids 2-6, 62-66, 107-111

### **Casein kinase II phosphorylation site.**

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

### **N-myristoylation site.**

amino acids 15-21, 74-80, 155-161

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 27-38



## **FIGURE 124**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTFPVVQEFESVELSCIITDSQTS
D
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARND
RK
EIDEIVIELTVQVKPVPVPCRVKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDS
RA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGYYCIASNDAGSARCEEQEMEVDNLNIGGI
IGG
VLVVLAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGD
FRHKSSFVI
```

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-30

#### **Transmembrane domain:**

amino acids 243-263

#### **N-glycosylation sites.**

amino acids 104-107, 192-195

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

#### **Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

#### **Tyrosine kinase phosphorylation site.**

amino acids 69-77

#### **N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267